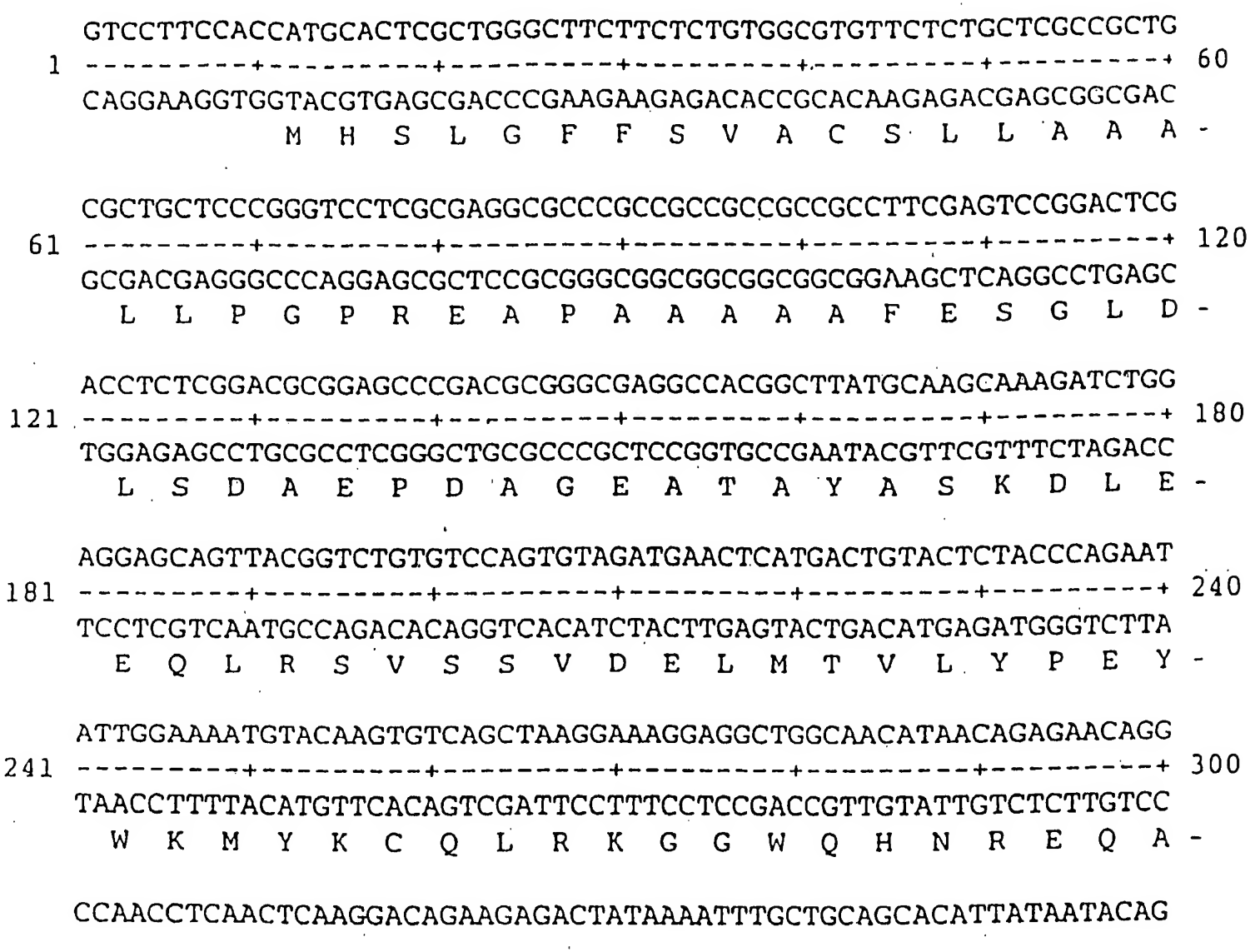


MATCH WITH FIG. 1B

FIG. 1A

MATCH WITH FIG. 1A

```
301 ---------+---------+---------+---------+---------+---------+ 360
    GGTTGGAGTTGAGTTCCTGTCTTCTCTGATATTTTAAACGACGTCGTGTAATATTATGTC
      N  L  N  S  R  T  E  E  T  I  K  F  A  A  A  H  Y  N  T  E -

    AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT
361 ---------+---------+---------+---------+---------+---------+ 420
    TCTAGAACTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA
      I  L  K  S  I  D  N  E  W  R  K  T  Q  C  M  P  R  E  V  C -

    GTATAGATGTGGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG
421 ---------+---------+---------+---------+---------+---------+ 480
    CATATCTACACCCCTTCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC
      I  D  V  G  K  E  F  G  V  A  T  N  T  F  F  K  P  P  C  V -

    TGTCCGTCTACAGATGTGGGGGTTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA
481 ---------+---------+---------+---------+---------+---------+ 540
    ACAGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT
      S  V  Y  R  C  G  G  C  C  N  S  E  G  L  Q  C  M  N  T  S -

    GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCA
541 ---------+---------+---------+---------+---------+---------+ 600
    CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCCGGGGT
      T  S  Y  L  S  K  T  L  F  E  I  T  V  P  L  S  Q  G  P  K -

    AACCAGTAACAATCAGTTTTGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG
601 ---------+---------+---------+---------+---------+---------+ 660
    TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTAC
      P  V  T  I  S  F  A  N  H  T  S  C  R  C  M  S  K  L  D  V -
```

MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

```
    TTTACAGACAAGTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC
661 ---------+---------+---------+---------+---------+---------+ 720
    AAATGTCTGTTCAAGTAAGGTAATAATCTGCAAGGGACGGTCGTTGTGATGGTGTCACAG
      Y  R  Q  V  H  S  I  I  R  R  S  L  P  A  T  L  P  Q  C  Q -

    AGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC
721 ---------+---------+---------+---------+---------+---------+ 780
    TCCGTCGCTTGTTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGTCTACGG
      A  A  N  K  T  C  P  T  N  Y  M  W  N  N  H  I  C  R  C  L -

    TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC
781 ---------+---------+---------+---------+---------+---------+ 840
    ACCGAGTCCTTCTAAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG
      A  Q  E  D  F  M  F  S  S  D  A  G  D  D  S  T  D  G  F  H -

    ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCAGTGTGTCTGCAGAG
841 ---------+---------+---------+---------+---------+---------+ 900
    TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC
      D  I  C  G  P  N  K  E  L  D  E  E  T  C  Q  C  V  C  R  A -

    CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT
901 ---------+---------+---------+---------+---------+---------+ 960
    GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTTCTTGATCTGTCTTTGAGTACGGTCA
      G  L  R  P  A  S  C  G  P  H  K  E  L  D  R  N  S  C  Q  C -

    GTGTCTGTAAAAACAAACTCTTCCCCAGCCAATGTGGGGCCAACCGAGAATTTGATGAAA
961 ---------+---------+---------+---------+---------+---------+ 1020
    CACAGACATTTTTGTTTGAGAAGGGGTCGGTTACACCCCGGTTGGCTCTTAAACTACTTT
```

MATCH WITH FIG. 1D

FIG. 1C

MATCH WITH FIG. 1C

```
      V  C  K  N  K  L  F  P  S  Q  C  G  A  N  R  E  F  D  E  N -

      ACACATGCCAGTGTGTATGTAAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA
1021  ---------+---------+---------+---------+---------+---------+---------+ 1080
      TGTGTACGGTCACACATACATTTTCTTGGACGGGGTCTTTAGTTGGGGATTTAGGACCTT
        T  C  Q  C  V  C  K  R  T  C  P  R  N  Q  P  L  N  P  G  K -

      AATGTGCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTTAAAAGGAAAGAAGTTCC
1081  ---------+---------+---------+---------+---------+---------+---------+ 1140
      TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCTTTCTTCAAGG
        C  A  C  E  C  T  E  S  P  Q  K  C  L  L  K  G  K  K  F  H -

      ACCACCAAACATGCAGCTGTTACAGACGGCCATGTACGAACCGCCAGAAGGCTTGTGAGC
1141  ---------+---------+---------+---------+---------+---------+---------+ 1200
      TGGTGGTTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG
        H  Q  T  C  S  C  Y  R  R  P  C  T  N  R  Q  K  A  C  E  P -

      CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCCTTCATATTGGCAAAGACCAC
1201  ---------+---------+---------+---------+---------+---------+---------+ 1260
      GTCCTAAAAGTATATCACTTCTTCACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG
        G  F  S  Y  S  E  E  V  C  R  C  V  P  S  Y  W  Q  R  P  Q -

      AAATGAGCTAAGATTGTACTGTTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT
```

MATCH WITH FIG. 1E

FIG. 1D

MATCH WITH FIG. 1D

```
1261 ---------+---------+---------+---------+---------+---------+ 1320
     TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA
       M   S   *

     TGCCACAGTAGAACTGTCTGTGAACAGAGAGACCCTTGTGGGTCCATGCTAACAAAGACA
1321 ---------+---------+---------+---------+---------+---------+ 1380
     ACGGTGTCATCTTGACAGACACTTGTCTCTCTGGGAACACCCAGGTACGATTGTTTCTGT

     AAAGTCTGTCTTTCCTGAACCATGTGGATAACTTTACAGAAATGGACTGGAGCTCATCTG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     TTTCAGACAGAAAGGACTTGGTACACCTATTGAAATGTCTTTACCTGACCTCGAGTAGAC

     CAAAAGGCCTCTTGTAAAGACTGGTTTTCTGCCAATGACCAAACAGCCAAGATTTTCCTC
1441 ---------+---------+---------+---------+---------+---------+ 1500
     GTTTTCCGGAGAACATTTCTGACCAAAAGACGGTTACTGGTTTGTCGGTTCTAAAAGGAG

     TTGTGATTTCTTTAAAAGAATGACTATATAATTTATTTCCACTAAAAATATTGTTTCTGC
1501 ---------+---------+---------+---------+---------+---------+ 1560
     AACACTAAAGAAATTTTCTTACTGATATATTAAATAAAGGTGATTTTTATAACAAAGACG

     ATTCATTTTTATAGCAACAACAATTGGTAAAACTCACTGTGATCAATATTTTTATATCAT
1561 ---------+---------+---------+---------+---------+---------+ 1620
     TAAGTAAAAATATCGTTGTTGTTAACCATTTTGAGTGACACTAGTTATAAAAATATAGTA

     GCAAAATATGTTTAAAATAAAATGAAAATTGTATTTATAAAAAAAAAAAAAAAA
1621 ---------+---------+---------+---------+---------+---- 1674
     CGTTTTATACAAATTTTATTTTACTTTTAACATAAATATTTTTTTTTTTTTTTT
```

FIG. 1E

```
  1  CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
     ---------+---------+---------+---------+---------+---------+

 71  AGATGAACTCATGACTGTACTCTACCCAGAATATTGGAAAATGTACAAGTGTCAGCTAAG
     ---------+---------+---------+---------+---------+---------+
               M  T  V  L  Y  P  E  Y  W  K  M  Y  K  C  Q  L  R

121  GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
     ---------+---------+---------+---------+---------+---------+
      K  G  G  W  Q  H  N  R  E  Q  A  N  L  N  S  R  T  E  E  T

181  TATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
     ---------+---------+---------+---------+---------+---------+
      I  K  F  A  A  A  H  Y  N  T  E  I  L  K  S  I  D  N  E  W

241  GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT
     ---------+---------+---------+---------+---------+---------+
      R  K  T  Q  C  M  P  R  E  V  C  I  D  V  G  K  E  F  G  V

301  CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCTG
     ---------+---------+---------+---------+---------+---------+
      A  T  N  T  F  F  K  P  P  C  V  S  V  Y  R  C  G  G  C  C
```

FIG. 2A

```
           .         .         .         .         .         .
361  CAATAGTGAGGGGCTGCAGTGCATGAACACCAGCACGAGCTACCTCAGCAAGACGTTATT
     ---------+---------+---------+---------+---------+---------+
      N  S  E  G  L  Q  C  M  N  T  S  T  S  Y  L  S  K  T  L  F

           .         .         .         .         .         .
421  TGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTGCCAATCA
     ---------+---------+---------+---------+---------+---------+
      E  I  T  V  P  L  S  Q  G  P  K  P  V  T  I  S  F  A  N  H

           .         .         .         .         .         .
481  CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG
     ---------+---------+---------+---------+---------+---------+
      T  S  C  R  C  M  S  K  L  D  V  Y  R  Q  V  H  S  I  I  R

           .         .         .         .         .         .
541  ACGTTCCCTGCCAGCAACACTACCACAGTGTCAGGCAGCGAACAAGACCTGCCCCACCAA
     ---------+---------+---------+---------+---------+---------+
      R  S  L  P  A  T  L  P  Q  C  Q  A  A  N  K  T  C  P  T  N

           .         .         .         .         .         .
601  TTACATGTGGAATAATCACATCTGCAGATGCCTGGCTCAGGAAGATTTTATGTTTTCCTC
     ---------+---------+---------+---------+---------+---------+
      Y  M  W  N  N  H  I  C  R  C  L  A  Q  E  D  F  M  F  S  S

           .         .         .         .         .         .
661  GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAAACAAGGAGCT
     ---------+---------+---------+---------+---------+---------+
      D  A  G  D  D  S  T  D  G  F  H  D  I  C  G  P  N  K  E  L
```

FIG. 2B

```
721  GGATGAAGAGACCTGTCAGTGTGTCTGCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACC
     ----------+---------+---------+---------+---------+---------+
      D  E  E  T  C  Q  C  V  C  R  A  G  L  R  P  A  S  C  G  P

781  CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAAAACAAACTCTTCCCCAG
     ----------+---------+---------+---------+---------+---------+
      H  K  E  L  D  R  N  S  C  Q  C  V  C  K  N  K  L  F  P  S

841  CCAATGTGGGGCCAACCGAGAATTTGATGAAAACACATGCCAGTGTGTATGTAAAAGAAC
     ----------+---------+---------+---------+---------+---------+
      Q  C  G  A  N  R  E  F  D  E  N  T  C  Q  C  V  C  K  R  T

901  CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCTGTGAATGTACAGAAAGTCC
     ----------+---------+---------+---------+---------+---------+
      C  P  R  N  Q  P  L  N  P  G  K  C  A  C  E  C  T  E  S  P

961  ACAGAAATGCTTGTTAAAAGGAAAGAAGTTCCACCACCAAACATGCAGCTGTTACAGACG
     ----------+---------+---------+---------+---------+---------+
      Q  K  C  L  L  K  G  K  K  F  H  H  Q  T  C  S  C  Y  R  R

1021 GCCATGTACGAACCGCCAGAAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG
     ----------+---------+---------+---------+---------+---------+
      P  C  T  N  R  Q  K  A  C  E  P  G  F  S  Y  S  E  E  V  C
```

FIG. 2C

```
1081  TCGTTGTGTCCCTTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTACTGTTTTCCA
      ---------+---------+---------+---------+---------+---------+
       R  C  V  P  S  Y  W  Q  R  P  Q  M  S

1141  GTTCATCGATTTTCTATTATGGAAAACTGTGTTGCCACAGTAGAACTGTCTGTGAACAGA
      ---------+---------+---------+---------+---------+---------+

1201  GAGACCCTTGTGGGTCCATGCTAACAAAGACAAAAGTCTGTCTTTCCTGAACCATGTGGA
      ---------+---------+---------+---------+---------+---------+

1261  TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCTCTTGTAAAGACTGGTTTT
      ---------+---------+---------+---------+---------+---------+

1321  CTGCCAATGACCAAACAGCCAAGATTTTCCTCTTGTGATTTCTTTAAAAGAATGACTATA
      ---------+---------+---------+---------+---------+---------+

1381  TAATTTATTTCCACTAAAAATATTGTTTCTGCATTCATTTTTATAGCAACAACAATTGGT
      ---------+---------+---------+---------+---------+---------+

1441  AAAACTCACTGTGATCAATATTTTTATATCATGCAAAATATGTTTAAAATAAAATGAAAA
      ---------+---------+---------+---------+---------+---------+

1501  TTGTATTATAAAAAAAAAAAAAAA
      ---------+---------+------
```

FIG. 2D

```
       1                                                 50
Pdgfa .MRTLACLLL LGCGYLAHVL AEEAEIPREV IERLARSQIH SIRDLQRLLE
Pdgfb MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLQRLLH
 Vegf .....MNFLL SWVHWSLALL LY........ .......... .LHHAKWSQA
Vegf2 .......MTV LYPEYWKMYK CQ........ .......... .LRKGGWQHN

      51                                                100
Pdgfa IDSVGSEDSL DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. .....EEAVP
Pdgfb GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI
 Vegf APMAE..... ......GGGQ NHHEVVKFMD .VYQR..... ..........
Vegf2 REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK..... ..........

      101                                               150
Pdgfa AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRCTGCC NTSSVKCQPS
Pdgfb AECKTRTEVF EISRRLIDRT NANFLVWPPC VEVQRCSGCC NNRNVQCRPT
 Vegf SYCHPIETLV DIFQEYPDEI ..EYIFKPSC VPLMRCGGCC NDEGLECVPT
Vegf2 TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

      151                                               200
Pdgfa RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECAC.... AT........
Pdgfb QVQLRPVQVR KIEIVRKKPI FKKATVTLED HLACKC.... ETVAAARPVT
 Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCECRPKK DRARQEKKSV
Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCRCMSKL DVYRQVHSII
```

FIG. 3A

```
      201                                                        250
Pdgfa ....TSLNPD YREEDTDVR. ..... ..... .....
Pdgfb RSPGGSQEQR AKTPQTRVTI RTVRVRRPPK GKHRKFKHTH DKTALKETLG
 Vegf RGK..... .GKGQKRKRK KSRYKSWSVY VGARCCLMPW SLPGPHP...
Vegf2 RRSLPATLPQ CQAANKTCPT NYMWNNHICR CLAQEDFMFS SDAGDDSTDG

      251                                                        300
Pdgfa ..... ..... ..... ..... .....
Pdgfb A..... ..... ..... ..... .....
 Vegf ....CGP... ..... .....CSE RRKHLFVQDP QTCKCSCKNT
Vegf2 FHDICGPNKE LDEETCQCVC RAGLRPASCG PHKEL...DR NSCQCVCKNK

      301                                                        350
Pdgfa ..... ..... ..... ..... .....
Pdgfb ..... ..... ..... ..... .....
 Vegf ..DSRCKARQ LELNERTCRC DKPRR..... ..... .....
Vegf2 LFPSQCGANR .EFDENTCQC VCKRTCPRNQ PLNPGKCACE CTESPQKCLL

      351                                                        398
Pdgfa ..... ..... ..... ..... .....
Pdgfb ..... ..... ..... ..... .....
 Vegf ..... ..... ..... ..... .....
Vegf2 KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCVPS YWQRPQMS
```

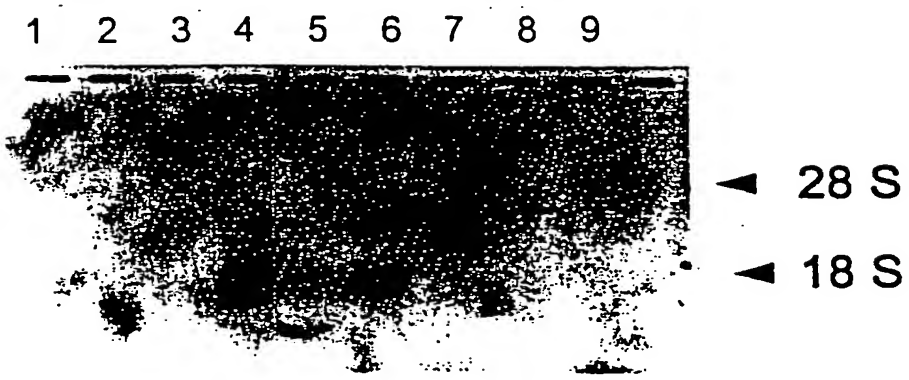
FIG. 3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLWING TABLE

	PDGFα	PDGFβ	VEGF	VEGF2
PDGFα				
PDGFβ	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

FIG.4

Expression of VEGF2 mRNA in Human Breast Tumor Cells

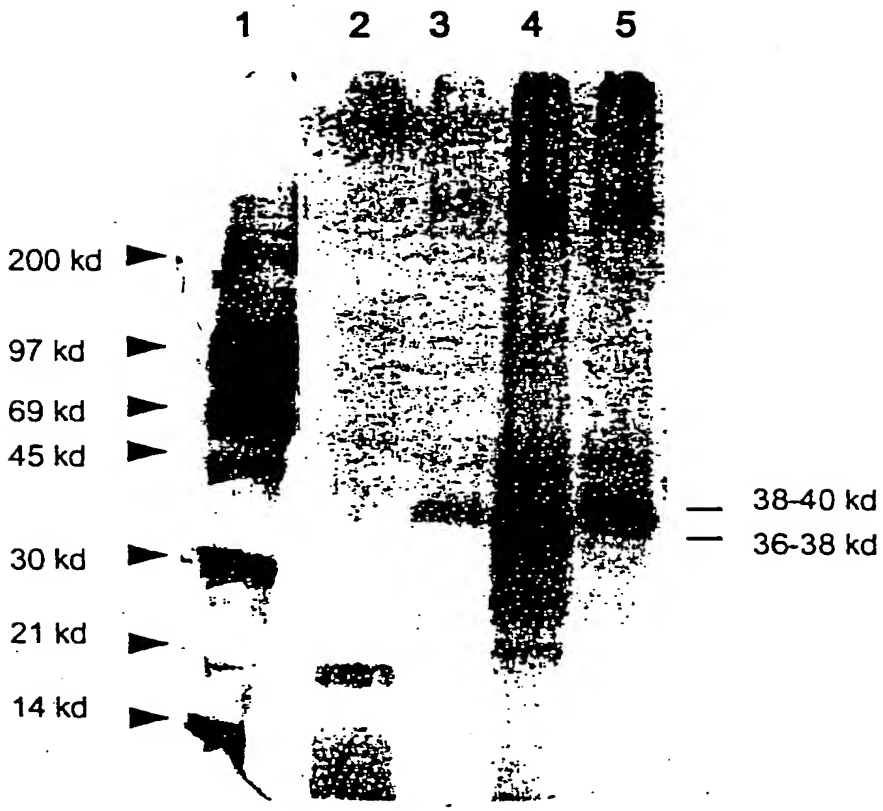


Lane 1. normal breast tissue
Lane 2. breast tumor tissue
Lane 3-9. breast tumor cell lines.

FIG.5

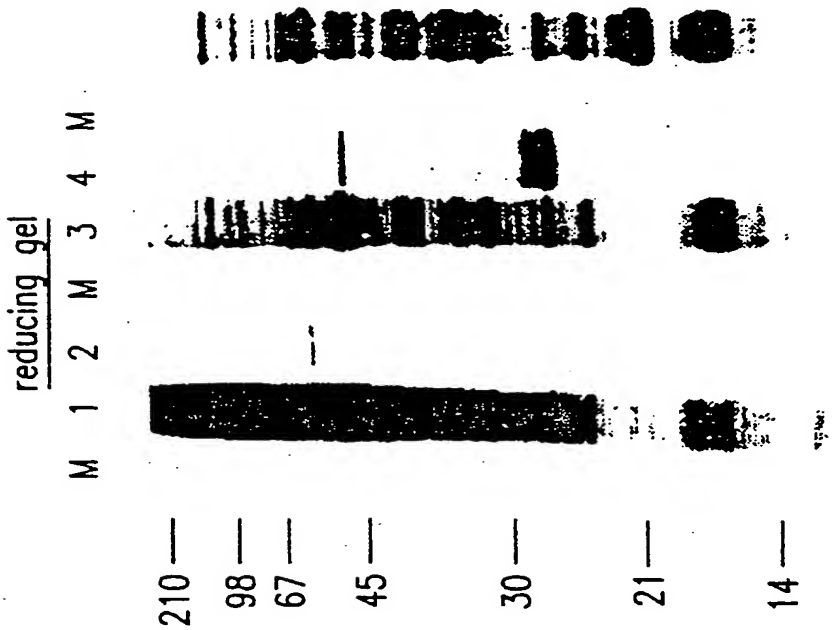
Expression of VEGF2 mRNA in human adult tissues.

FIG.6



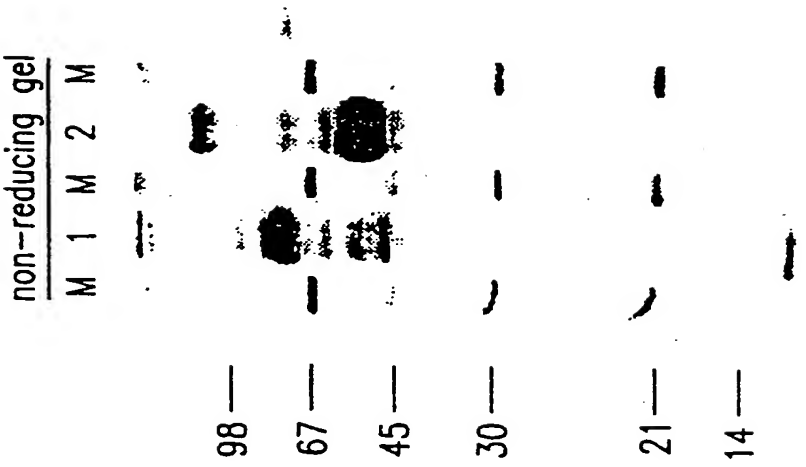
Lane 1: 14-C and rainbow M.W. marker
Lane 2: FGF control
Lane 3: VEGF2 (M13-reverse $ forward primers)
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

FIG.7



Lane M: Marker
Lane 1: vector Cytoplasm
Lane 2: vector medium
Lane 3: VEGF2 Cytoplasm
Lane 4: VEGF2 medium

FIG.8B



Lane M Marker
Lane 1 vector medium
Lane 2 VEGF2 medium

FIG.8A

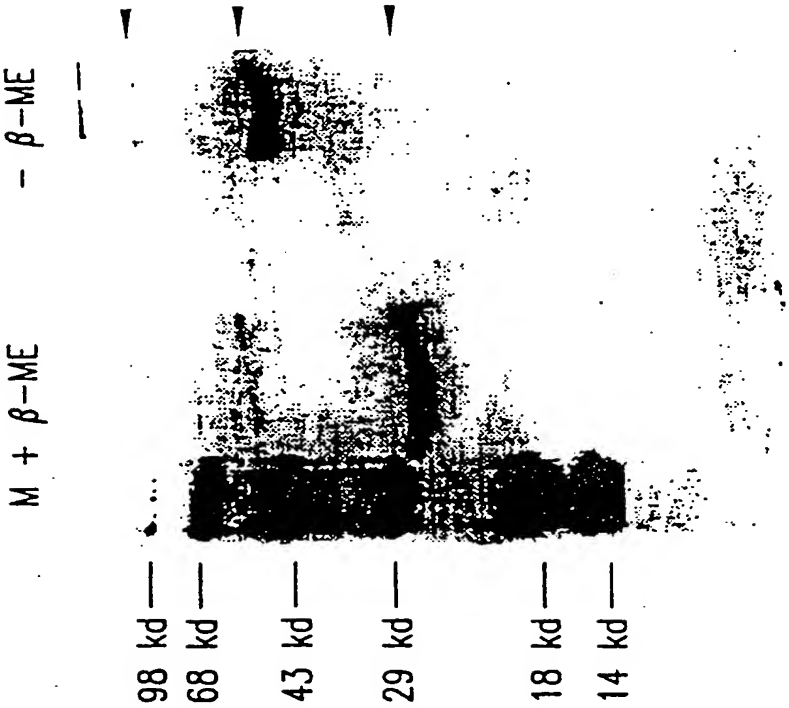
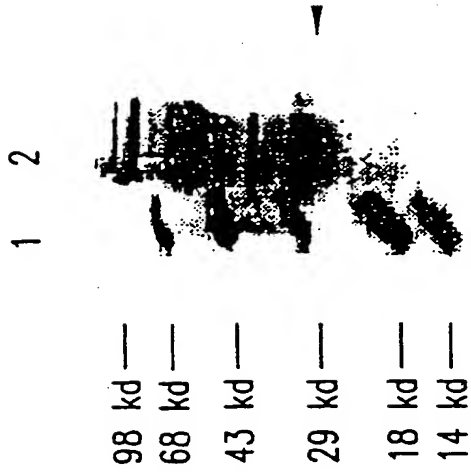


FIG.10



Lane 1: Molelular weight marker
Lane 2: Precipitates containing VEGF2.

FIG.9

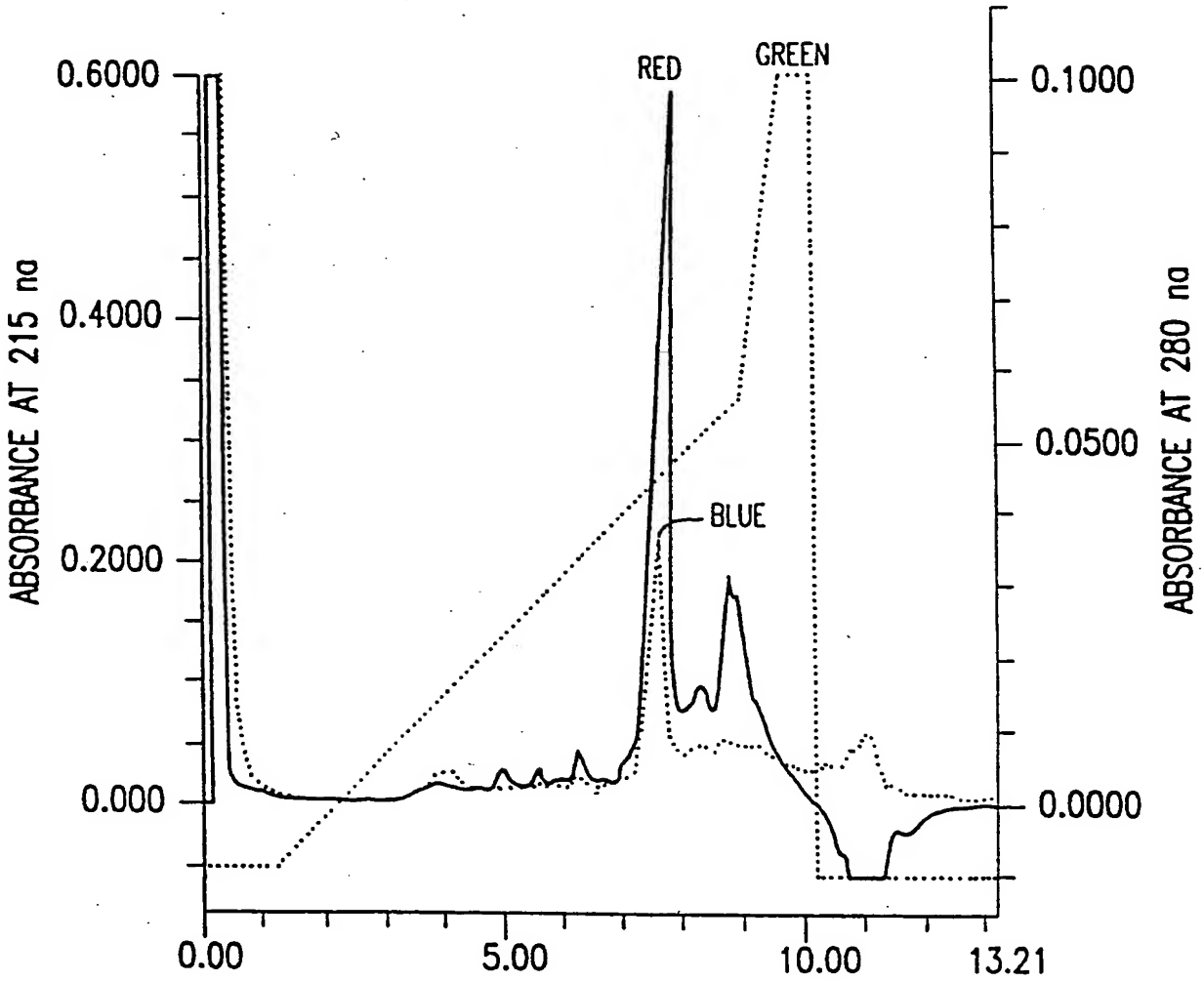


FIG. 11

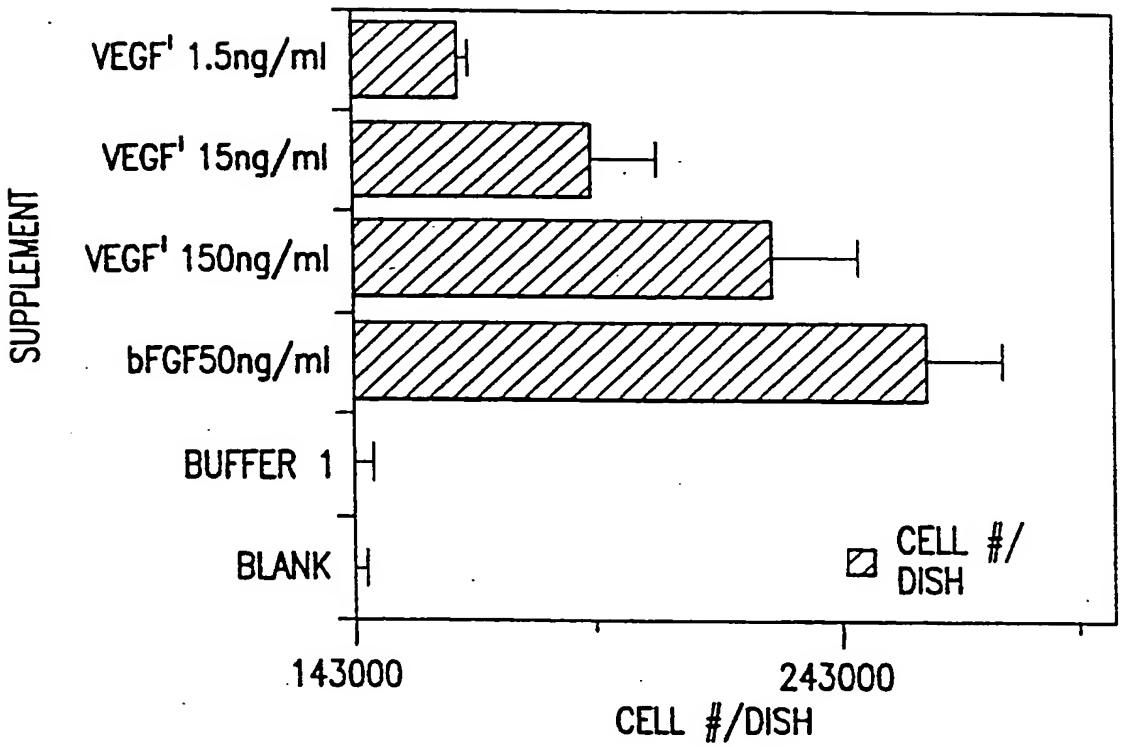

VEGF' 1.5ng/ml
VEGF' 15ng/ml
VEGF' 150ng/ml
bFGF50ng/ml
BUFFER 1
BLANK
SUPPLEMENT
CELL #/ DISH
143000
243000
CELL #/DISH

FIG.12

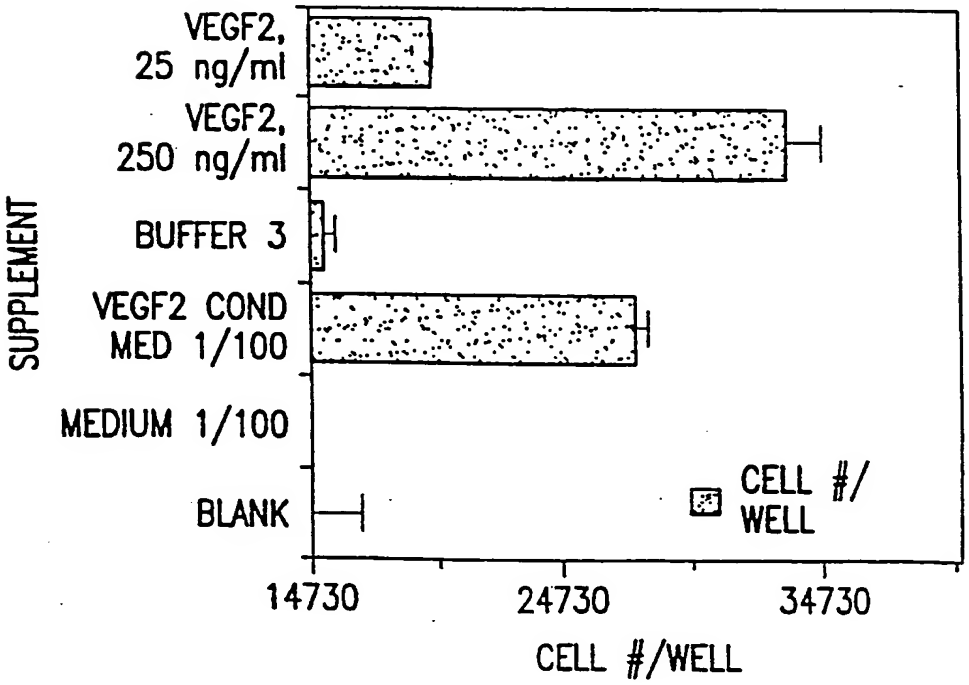

VEGF2, 25 ng/ml
VEGF2, 250 ng/ml
BUFFER 3
VEGF2 COND MED 1/100
MEDIUM 1/100
BLANK
SUPPLEMENT
CELL #/ WELL
14730
24730
34730
CELL #/WELL

FIG.13

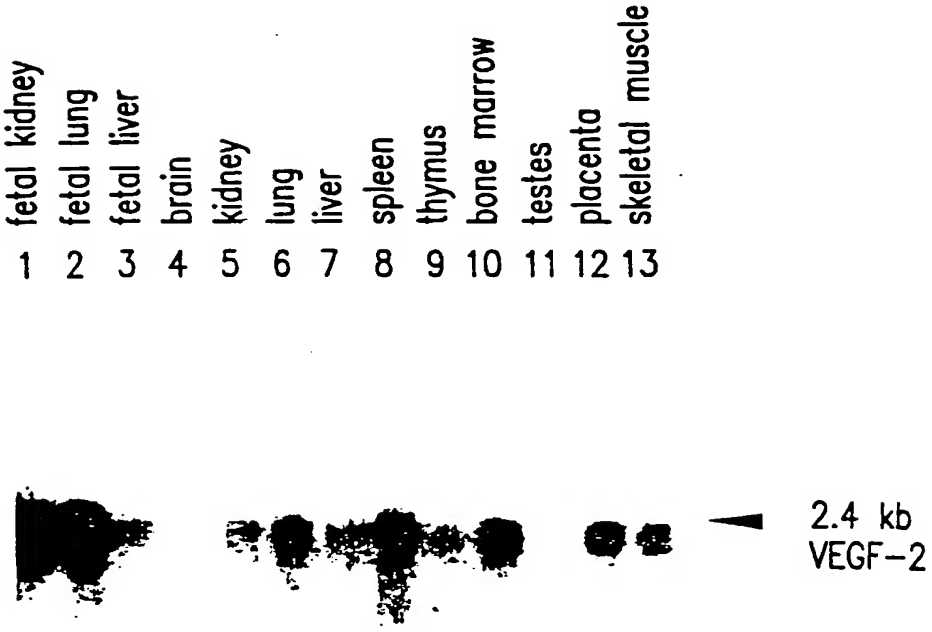


FIG.14A

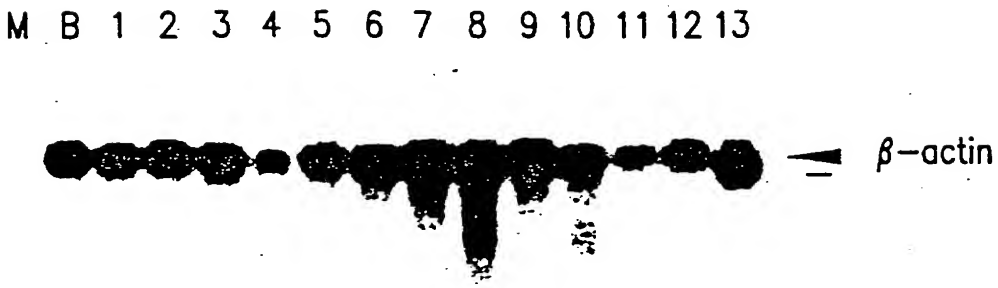


FIG.14B

1. Molecular Weight Marker
2. umbelical vein endothelial cells
3. aortic smooth muscle cells
4. Dermal fibroblast

FIG.15

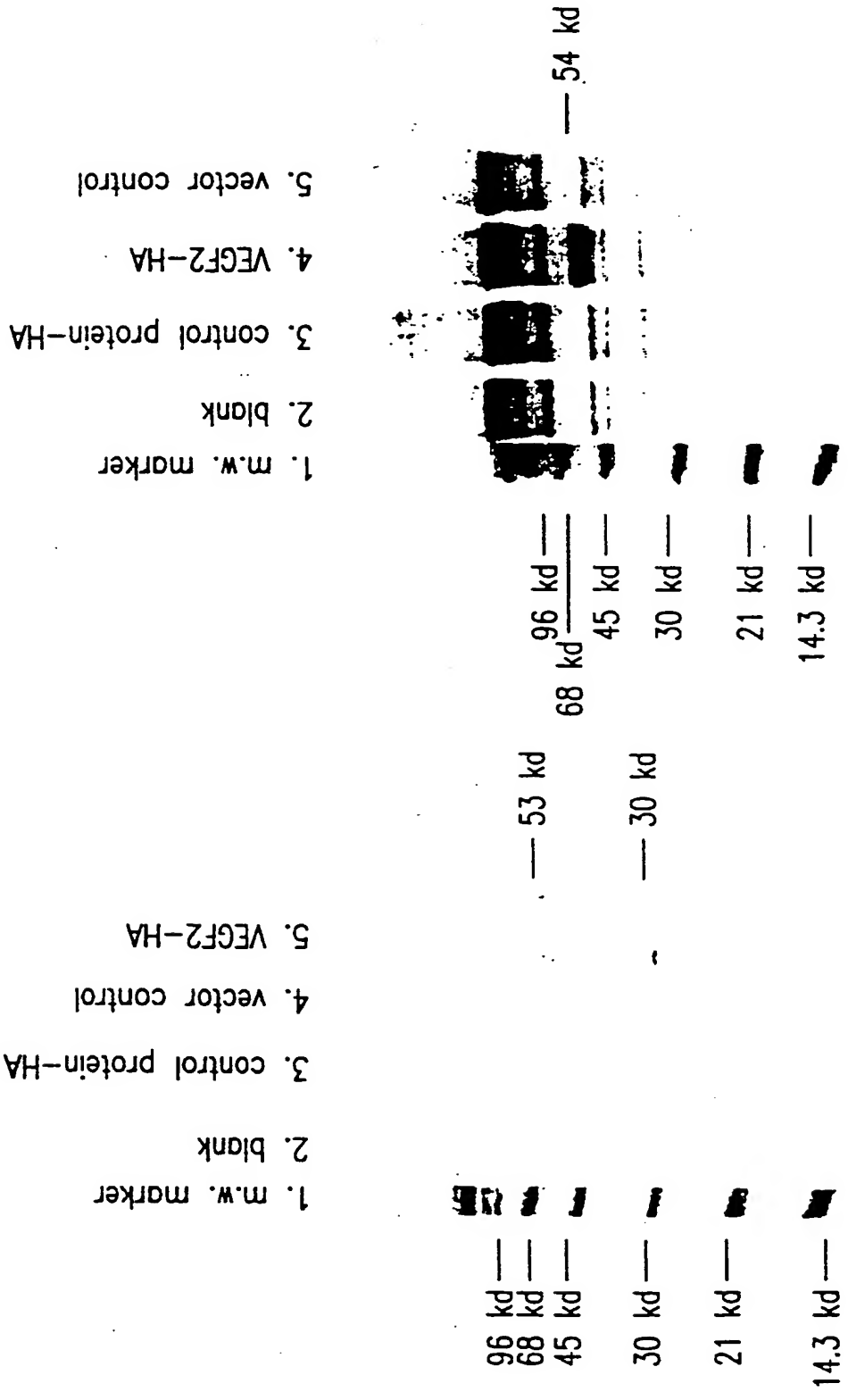


FIG.16A

FIG.16B

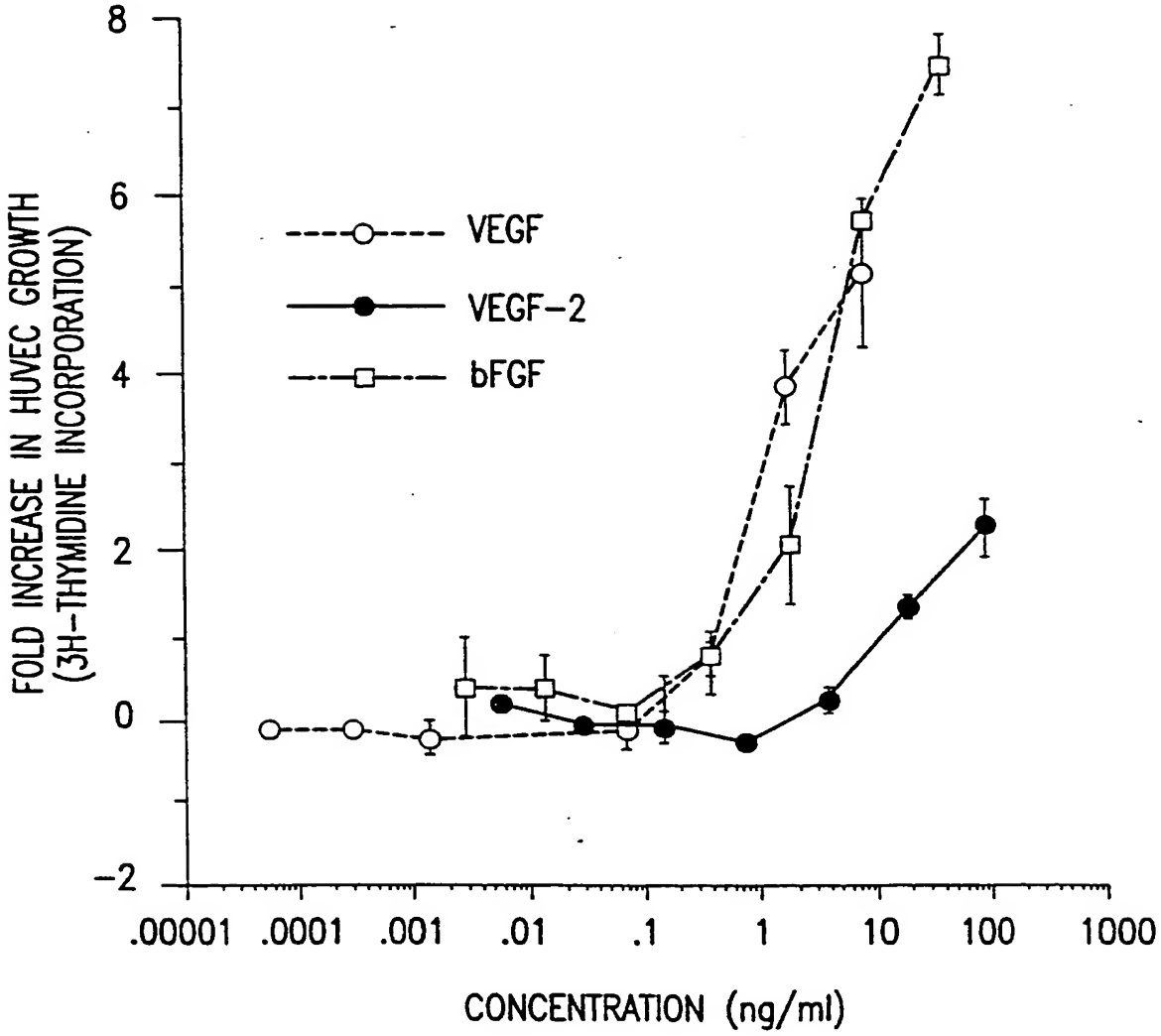

8
6
4
2
0
−2
FOLD INCREASE IN HUVEC GROWTH
(3H-THYMIDINE INCORPORATION)
VEGF
VEGF-2
bFGF
.00001
.0001
.001
.01
.1
1
10
100
1000
CONCENTRATION (ng/ml)

FIG.17

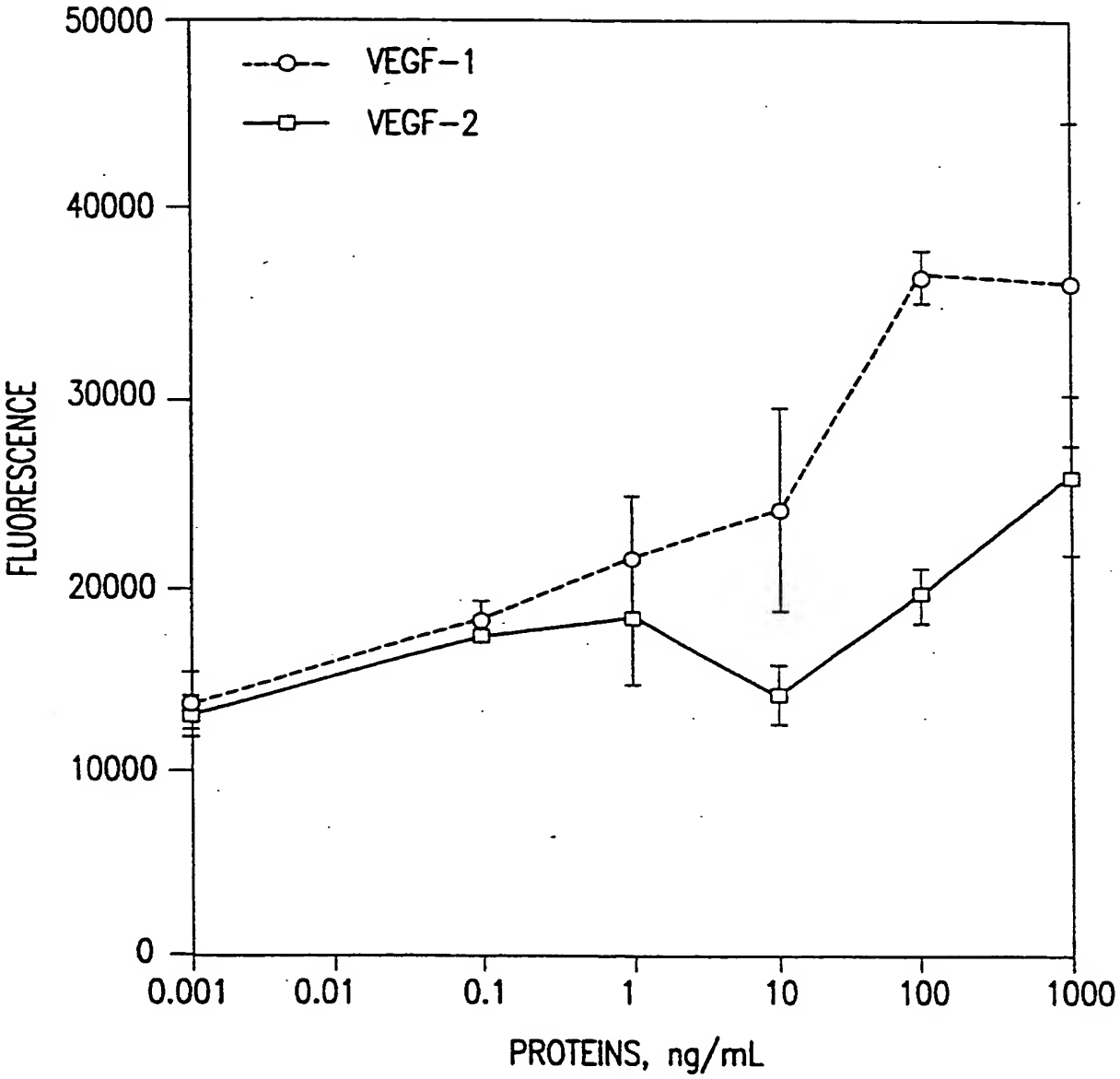

50000
40000
30000
20000
10000
0
FLUORESCENCE
VEGF-1
VEGF-2
0.001
0.01
0.1
1
10
100
1000
PROTEINS, ng/mL

FIG.18

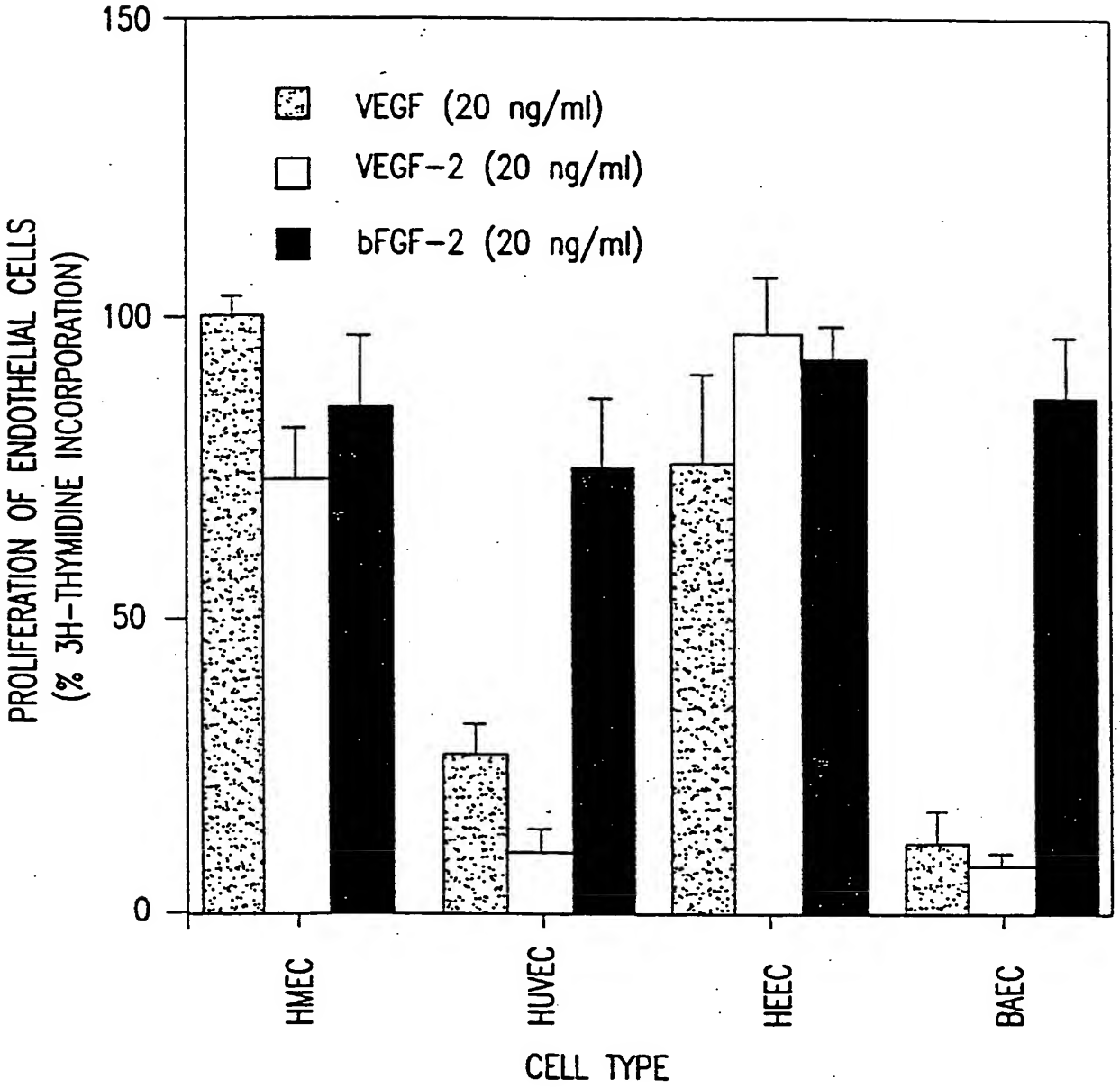

150
100
50
0
VEGF (20 ng/ml)
VEGF-2 (20 ng/ml)
bFGF-2 (20 ng/ml)
PROLIFERATION OF ENDOTHELIAL CELLS
(% 3H-THYMIDINE INCORPORATION)
HMEC
HUVEC
HEEC
BAEC
CELL TYPE

FIG.19

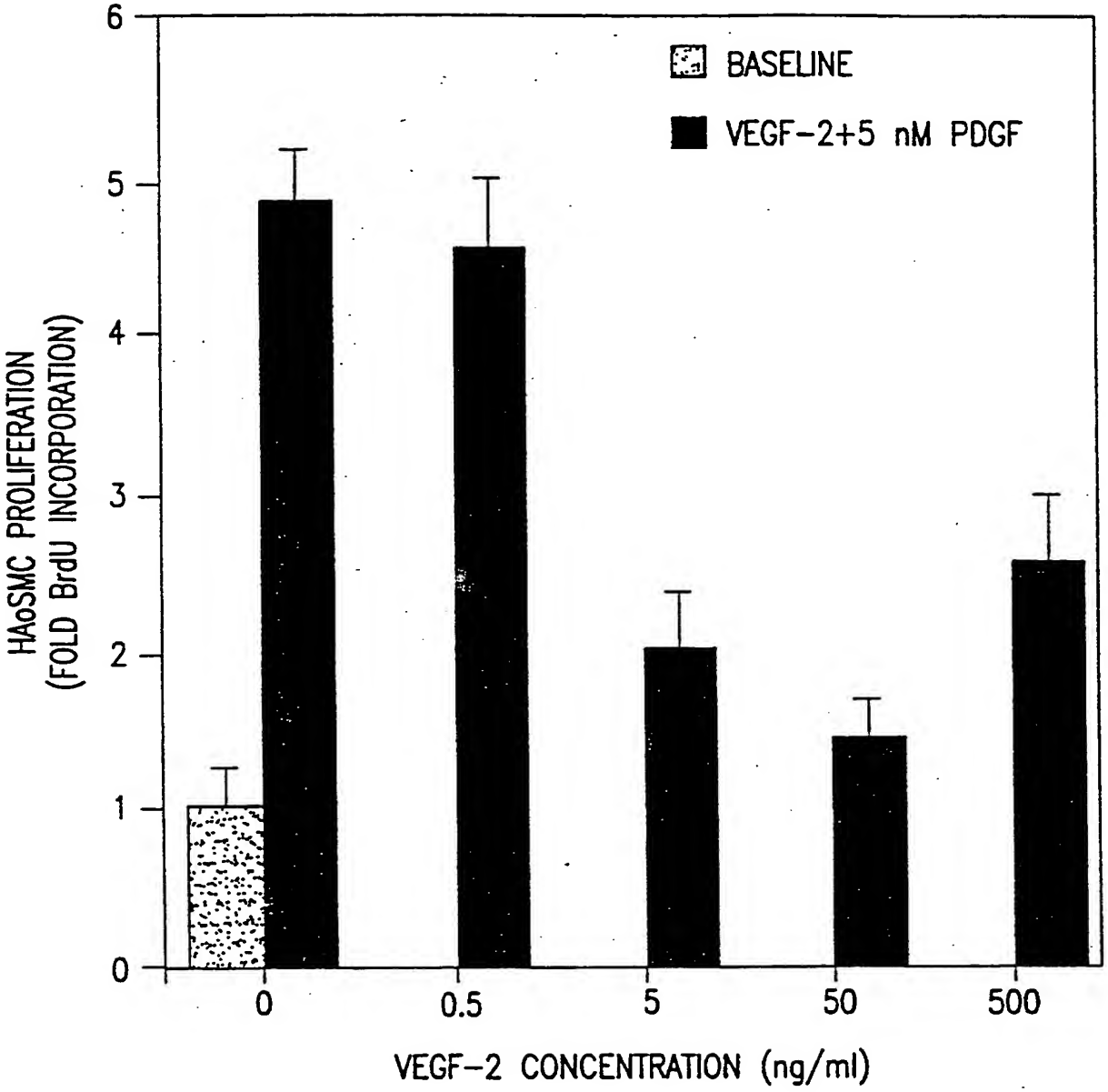

BASELINE
VEGF-2+5 nM PDGF
HAoSMC PROLIFERATION
(FOLD BrdU INCORPORATION)
0
1
2
3
4
5
6
0
0.5
5
50
500
VEGF-2 CONCENTRATION (ng/ml)

FIG.20A

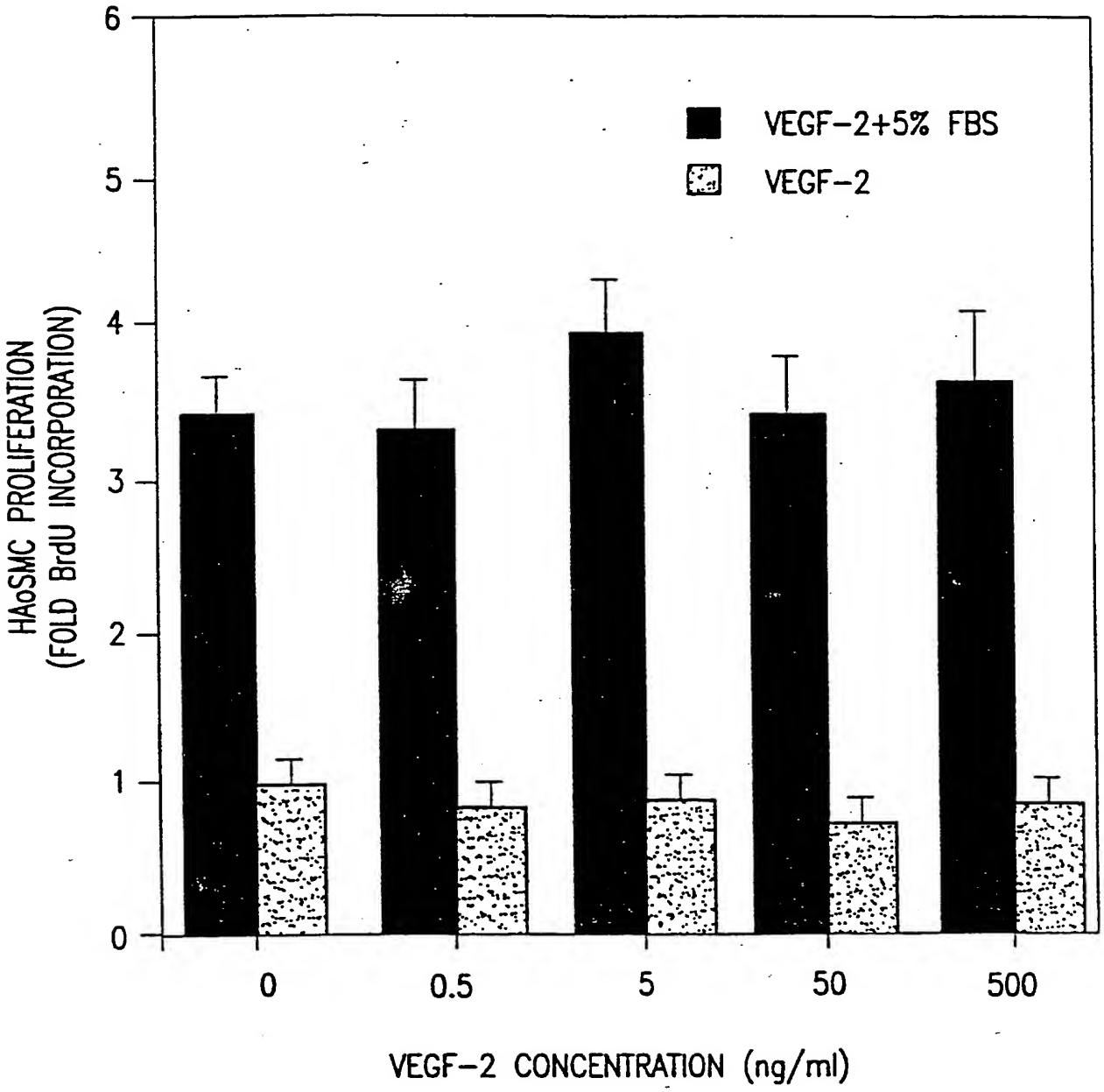

6
5
4
3
2
1
0
VEGF-2+5% FBS
VEGF-2
HAoSMC PROLIFERATION
(FOLD BrdU INCORPORATION)
0
0.5
5
50
500
VEGF-2 CONCENTRATION (ng/ml)

FIG.20B

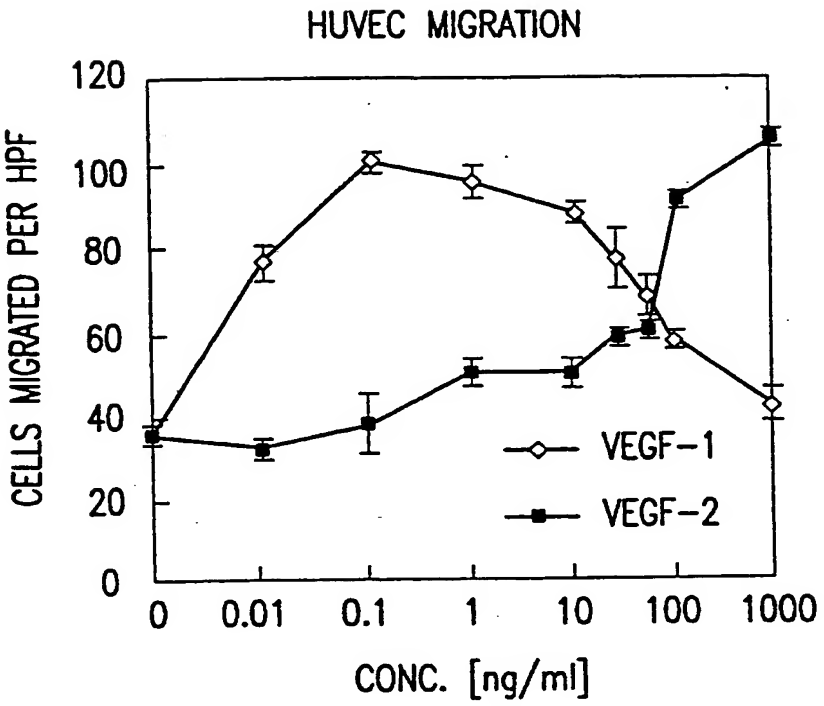


FIG.21A

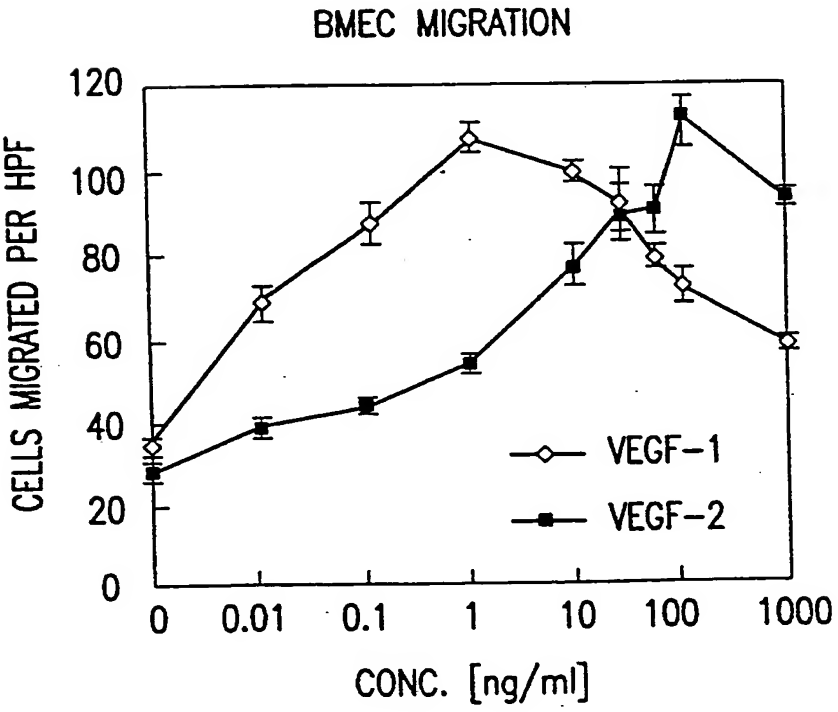


FIG.21B

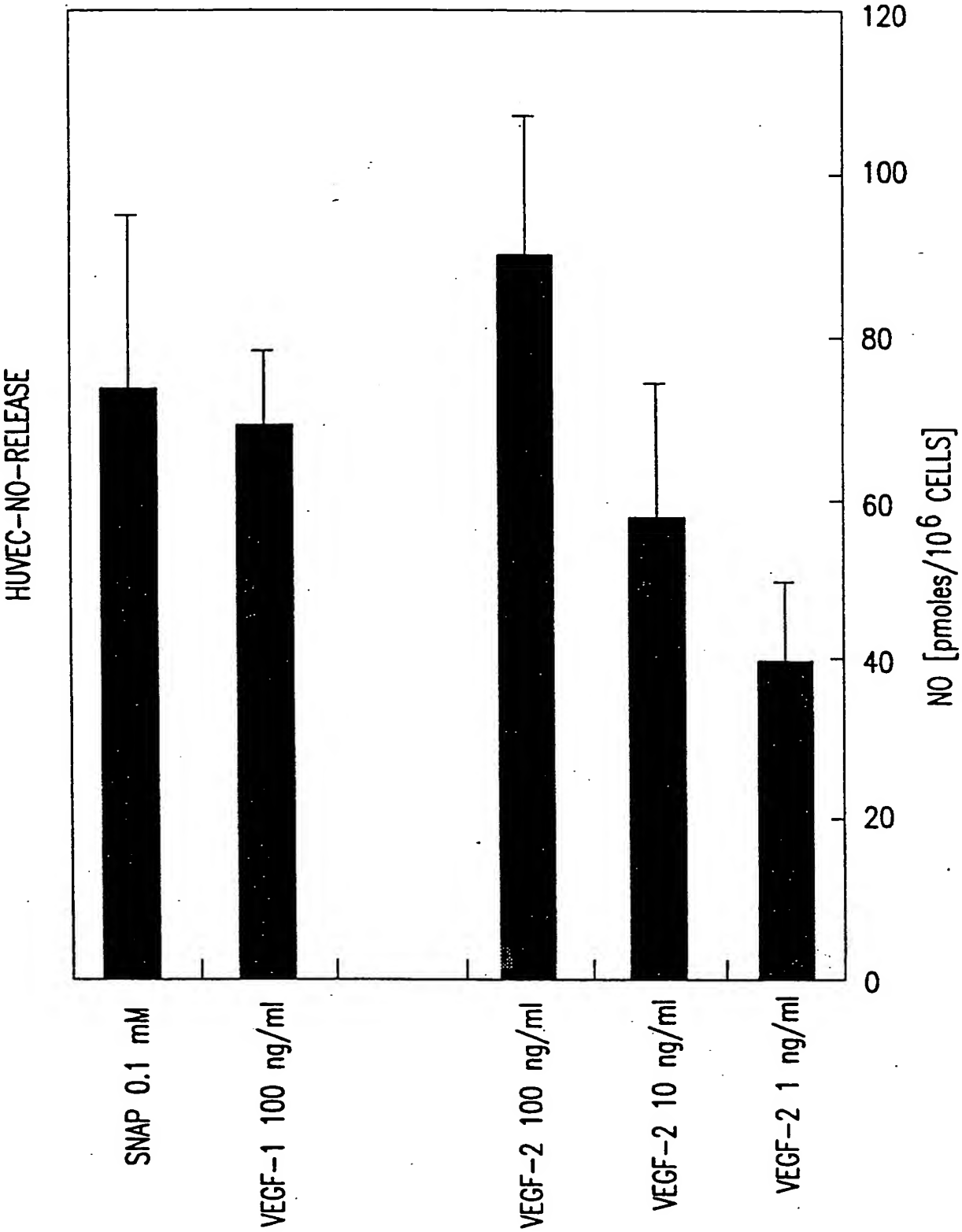

HUVEC-NO-RELEASE
NO [pmoles/10^6 CELLS]
120
100
80
60
40
20
0
SNAP 0.1 mM
VEGF-1 100 ng/ml
VEGF-2 100 ng/ml
VEGF-2 10 ng/ml
VEGF-2 1 ng/ml

FIG.22

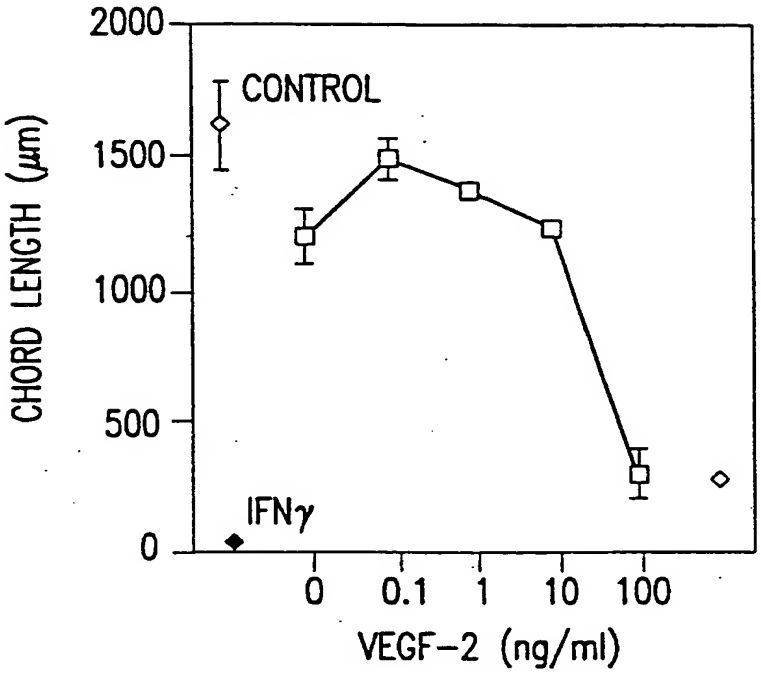

2000
1500
1000
500
0
CHORD LENGTH (μm)
CONTROL
IFNγ
0
0.1
1
10
100
VEGF-2 (ng/ml)

FIG.23

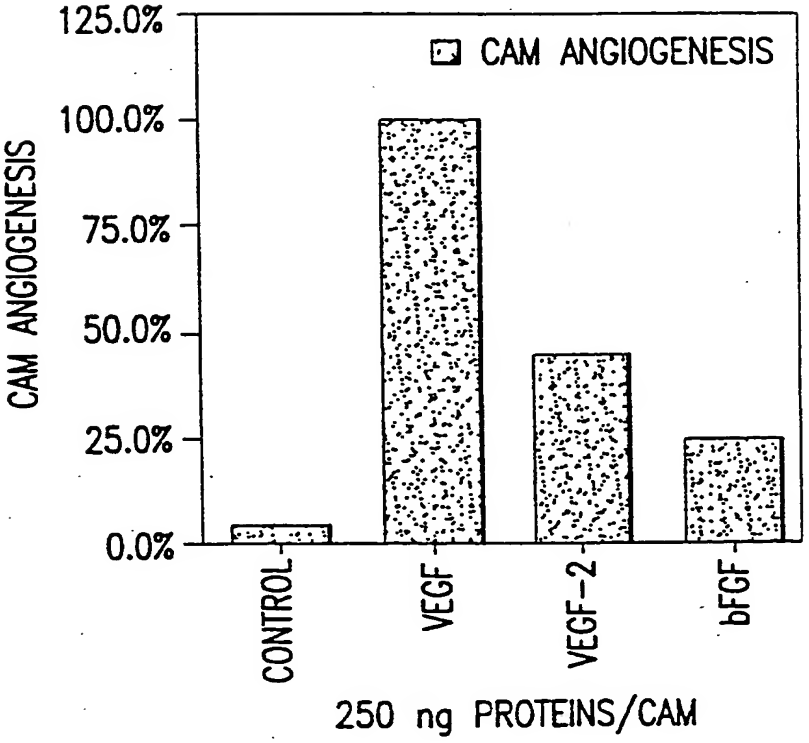

125.0%
100.0%
75.0%
50.0%
25.0%
0.0%
CAM ANGIOGENESIS
CAM ANGIOGENESIS
CONTROL
VEGF
VEGF-2
bFGF
250 ng PROTEINS/CAM

FIG.24

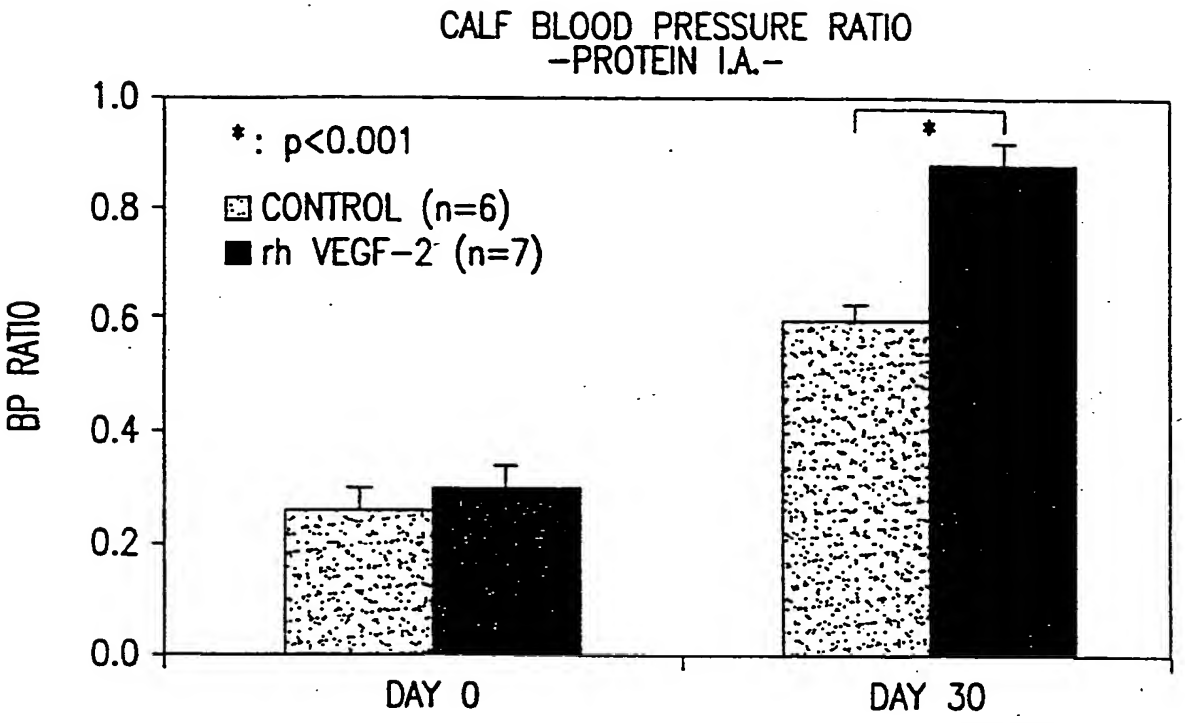


FIG.25A

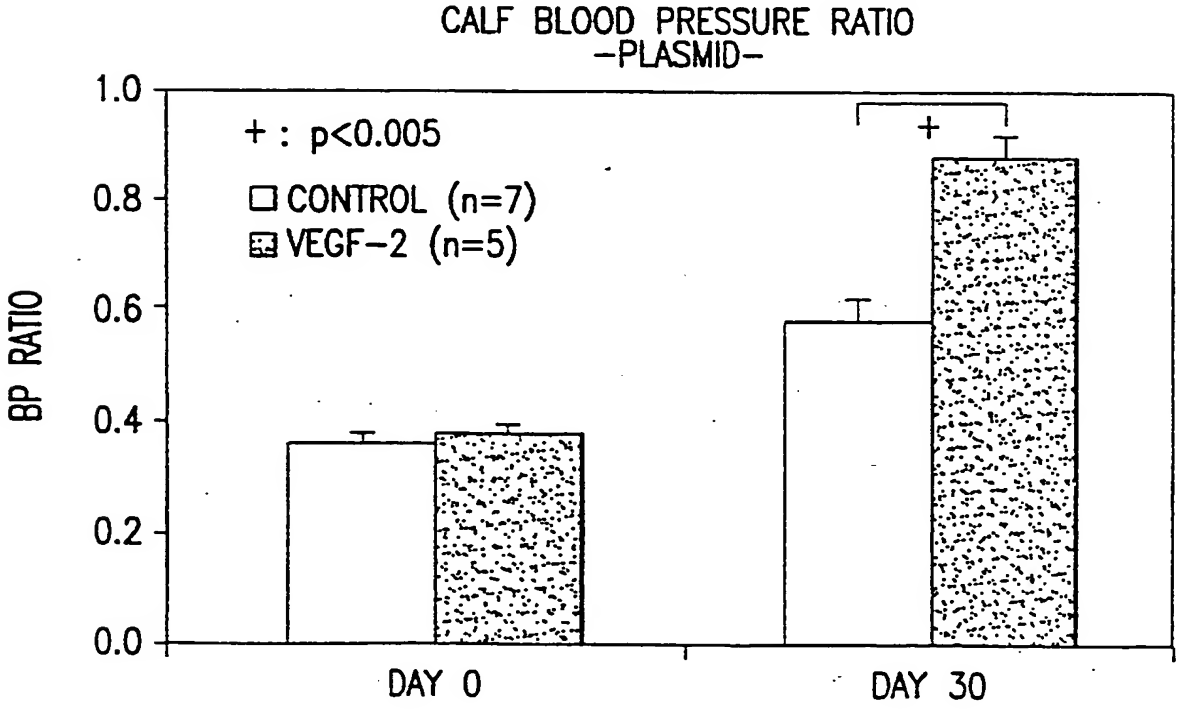


FIG.25B

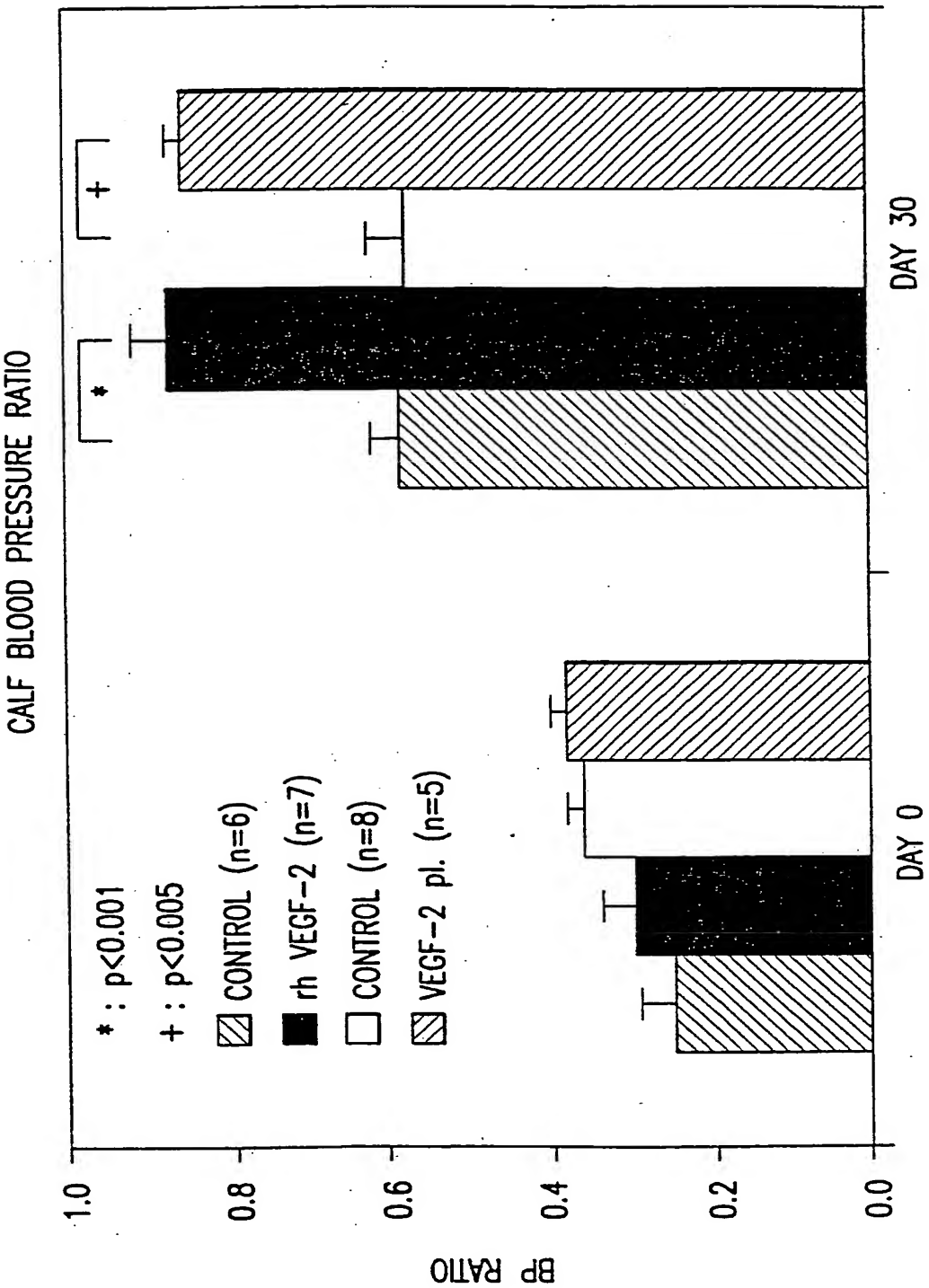

CALF BLOOD PRESSURE RATIO
*: p<0.001
+: p<0.005
CONTROL (n=6)
rh VEGF-2 (n=7)
CONTROL (n=8)
VEGF-2 pl. (n=5)
DAY 0
DAY 30
BP RATIO
1.0
0.8
0.6
0.4
0.2
0.0

FIG.25C

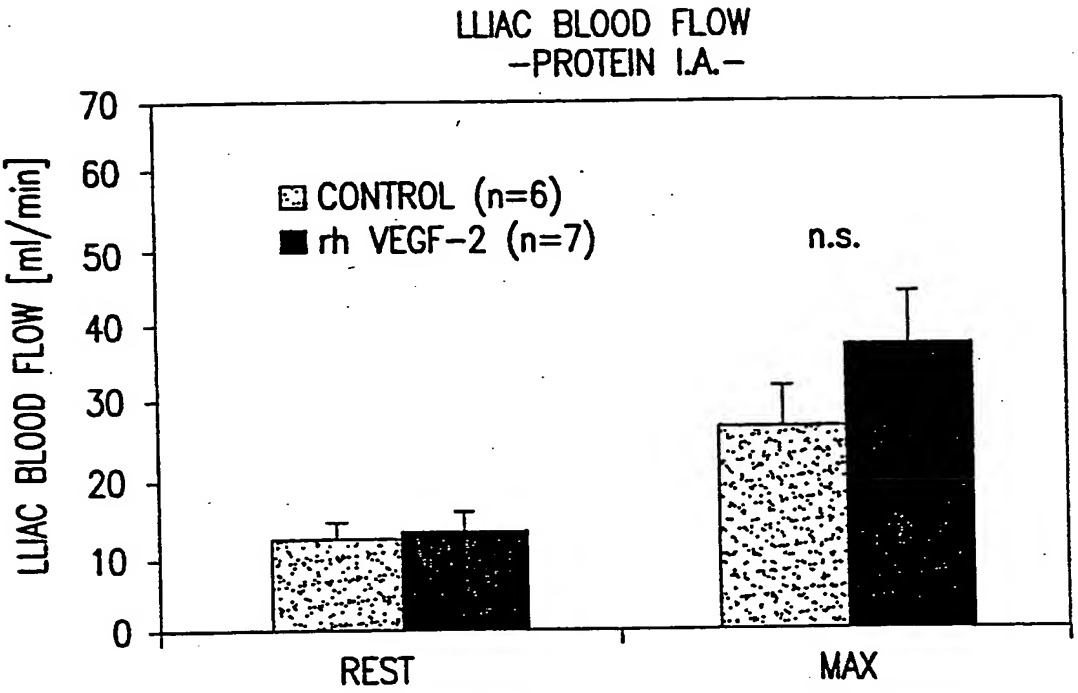


FIG.25D

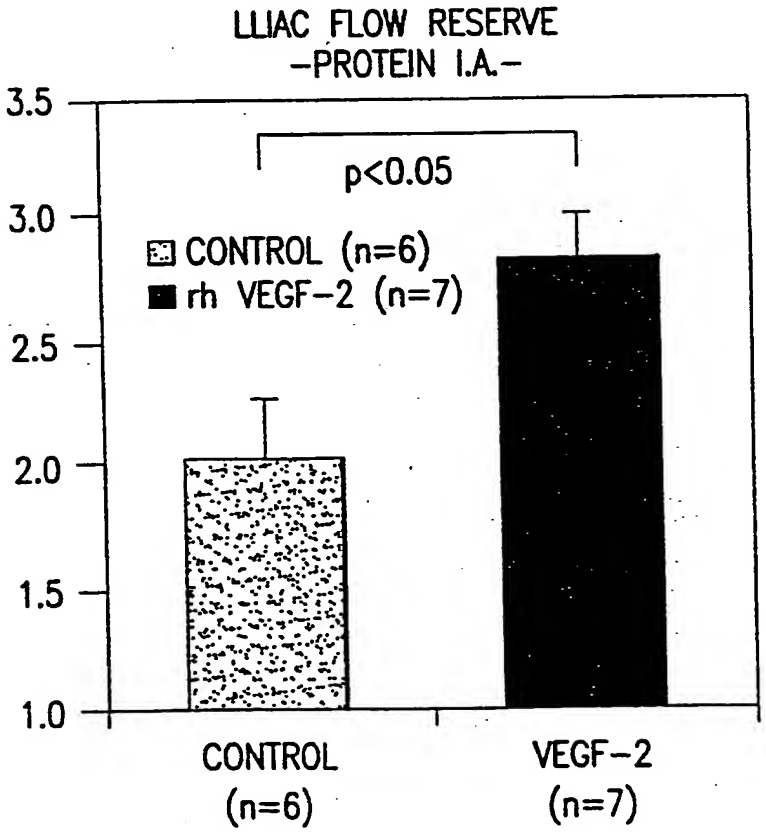


FIG.25E

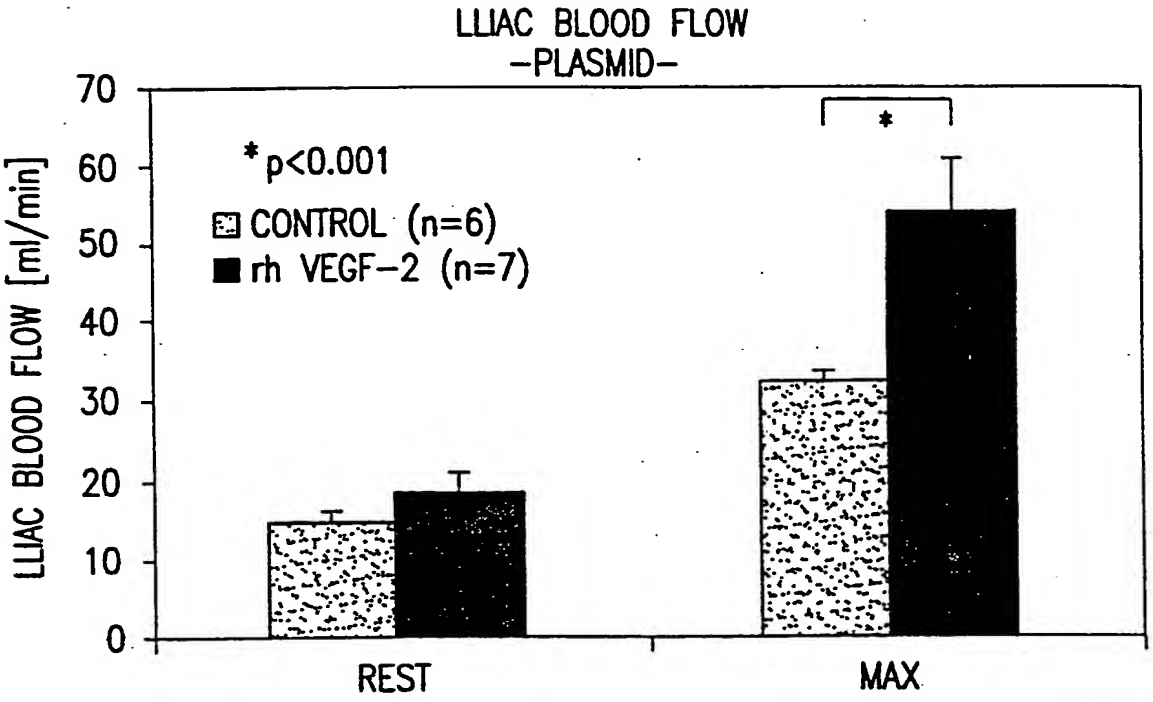


FIG.25F

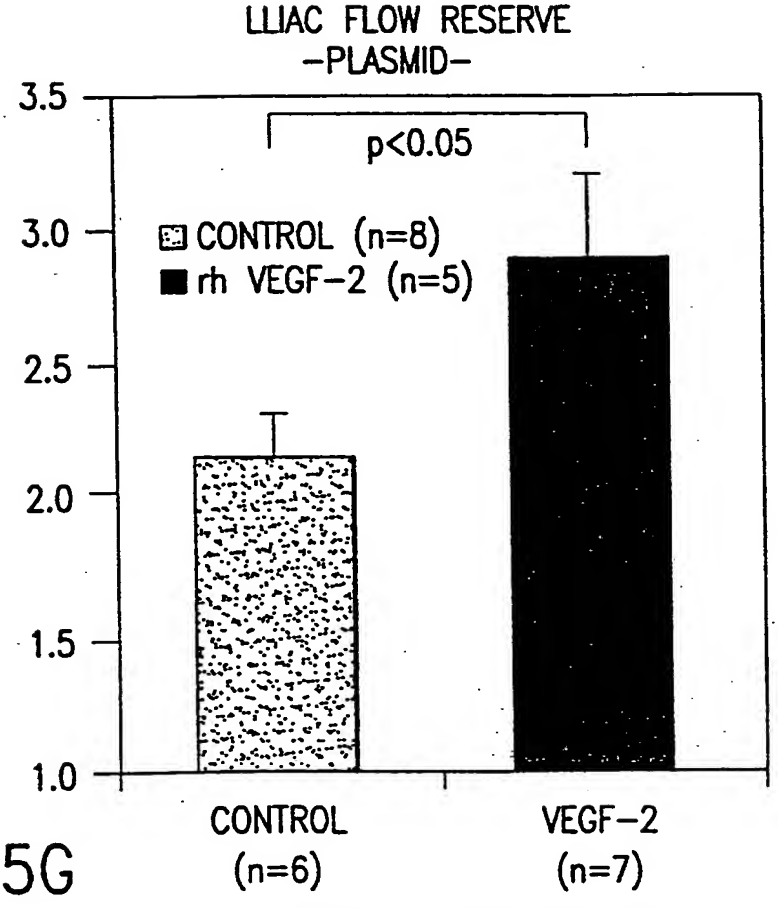


FIG.25G

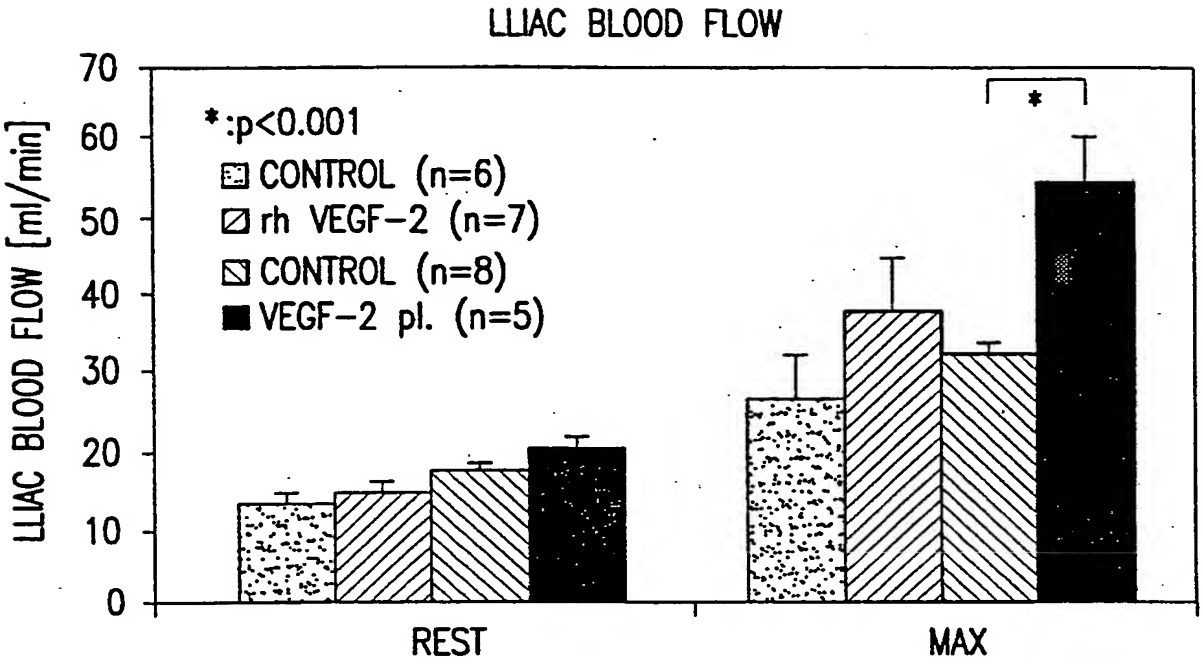


FIG.25H

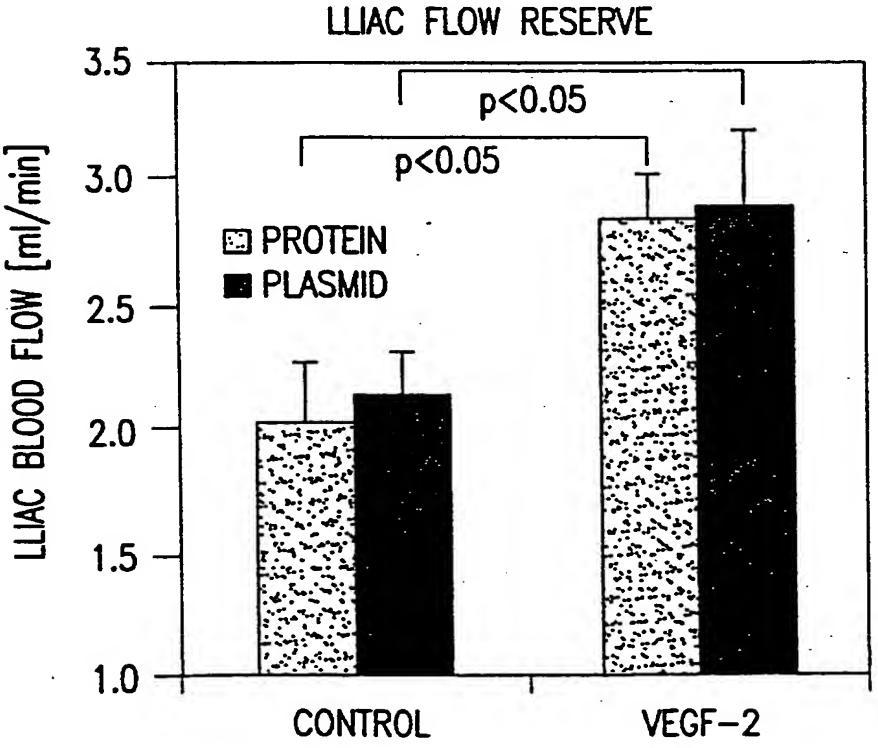


FIG.25I

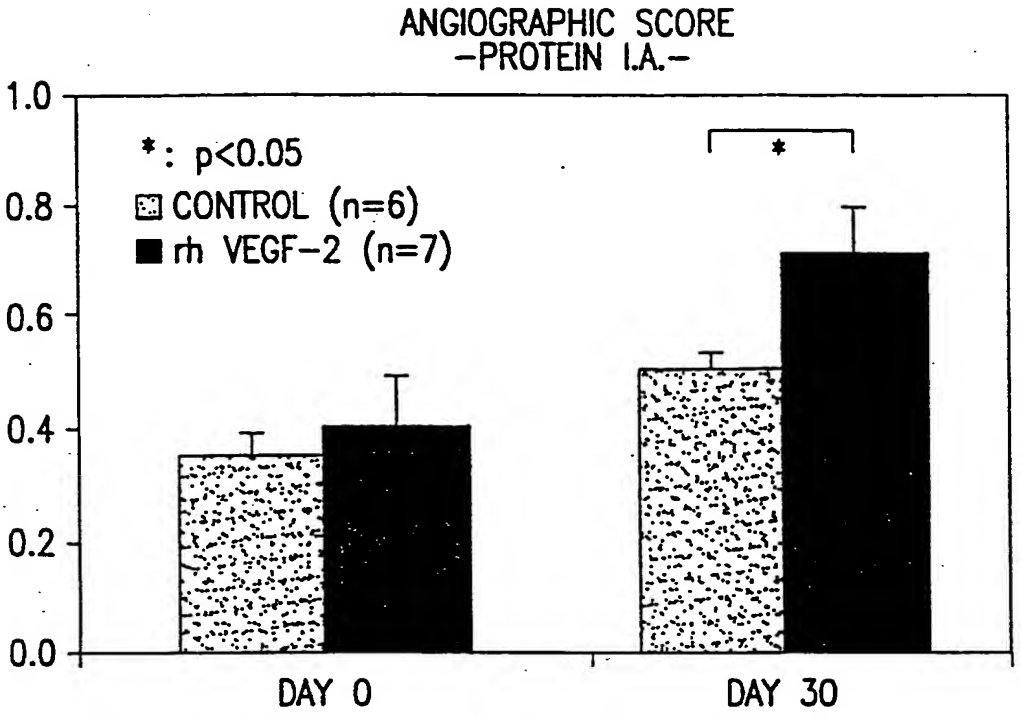


FIG.25J

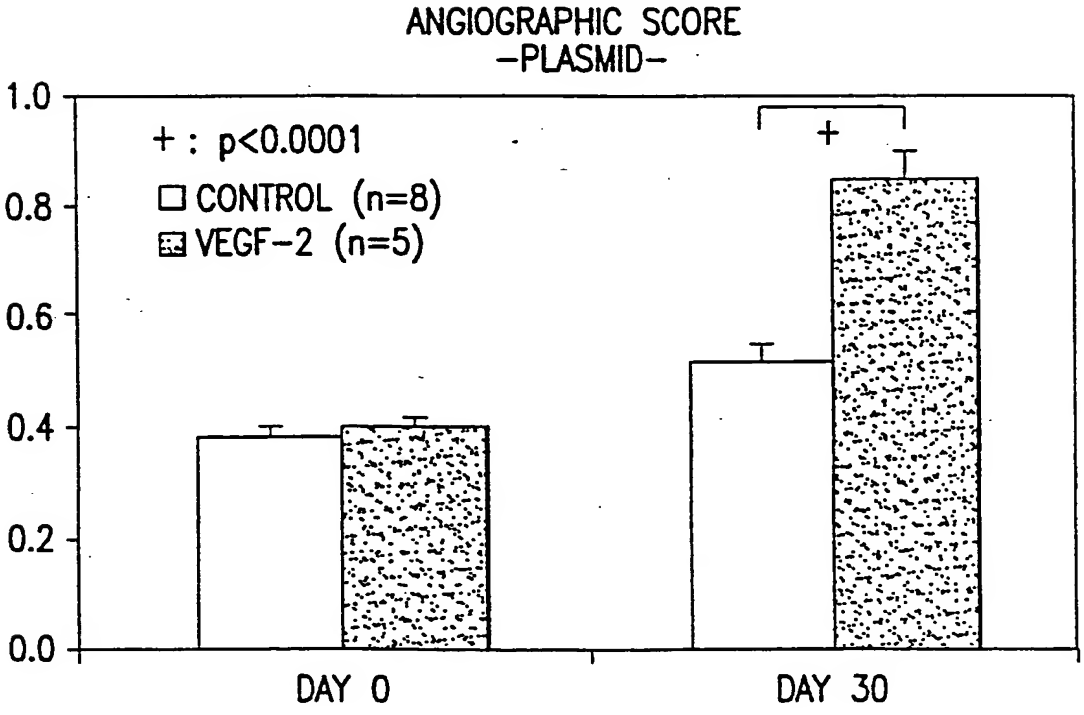


FIG.25K

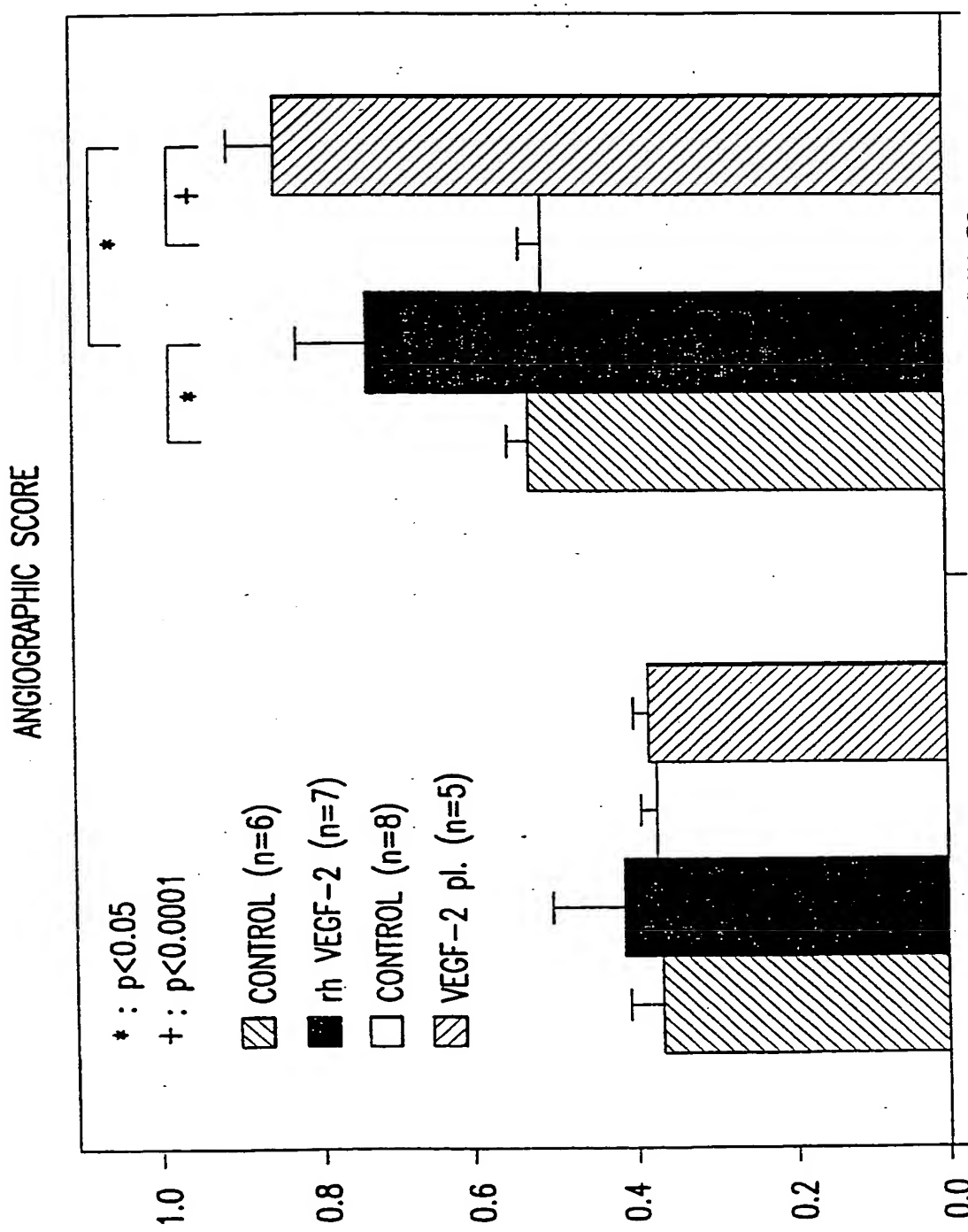

ANGIOGRAPHIC SCORE
1.0
0.8
0.6
0.4
0.2
0.0
*: p<0.05
+: p<0.0001
CONTROL (n=6)
rh VEGF-2 (n=7)
CONTROL (n=8)
VEGF-2 pl. (n=5)
DAY 0
DAY 30
*
*
+

FIG.25L

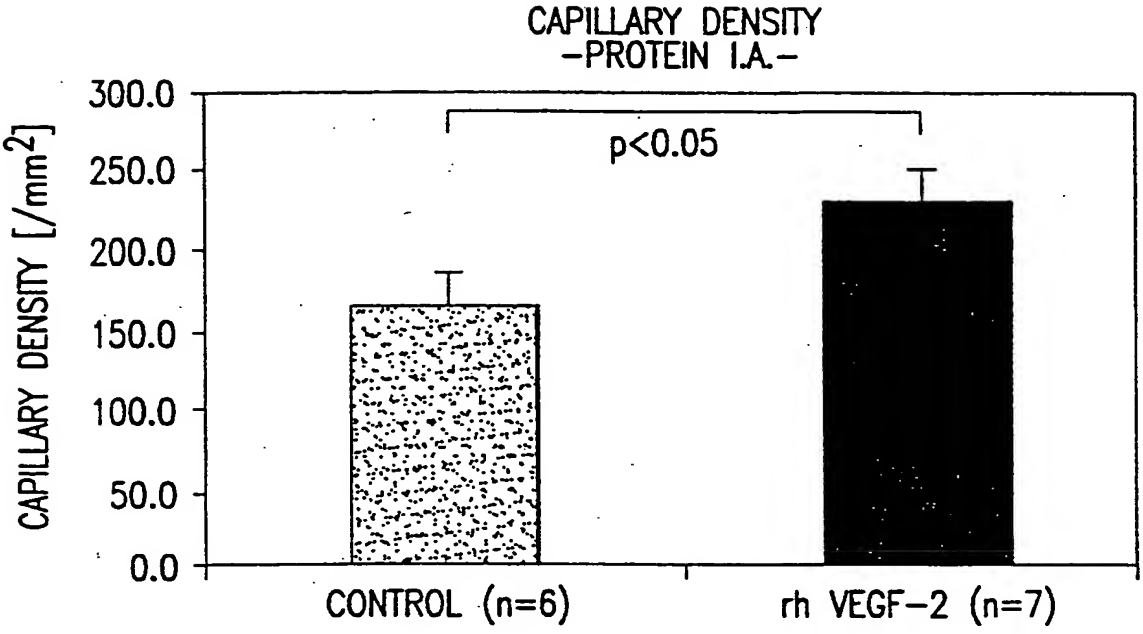


FIG.25M

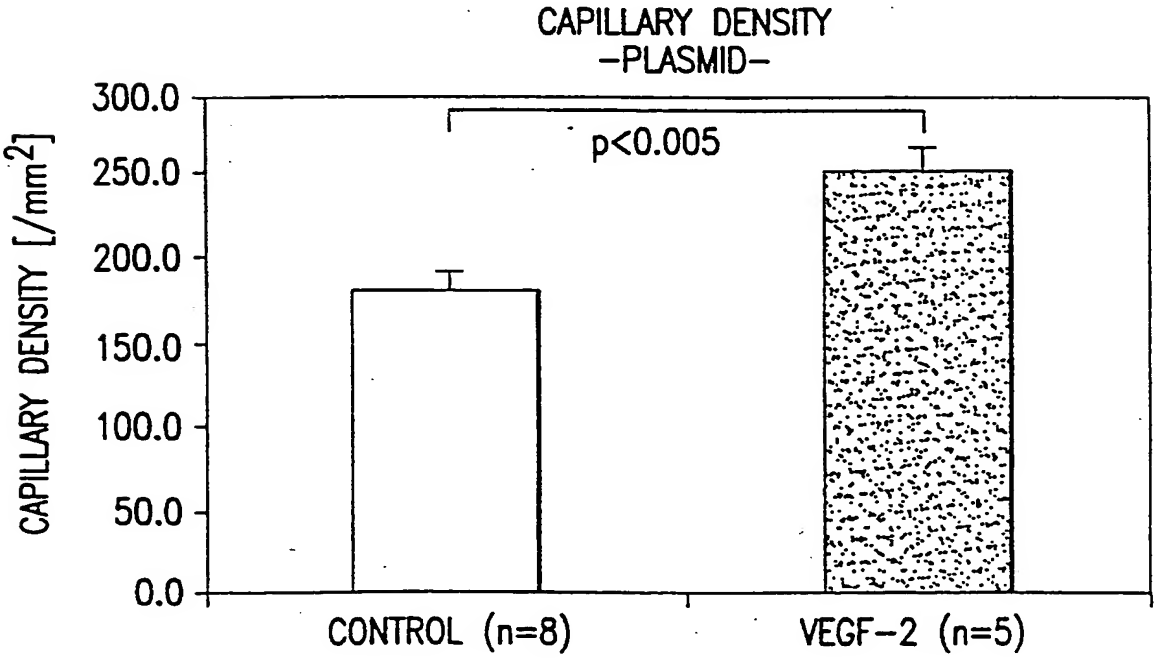


FIG.25N

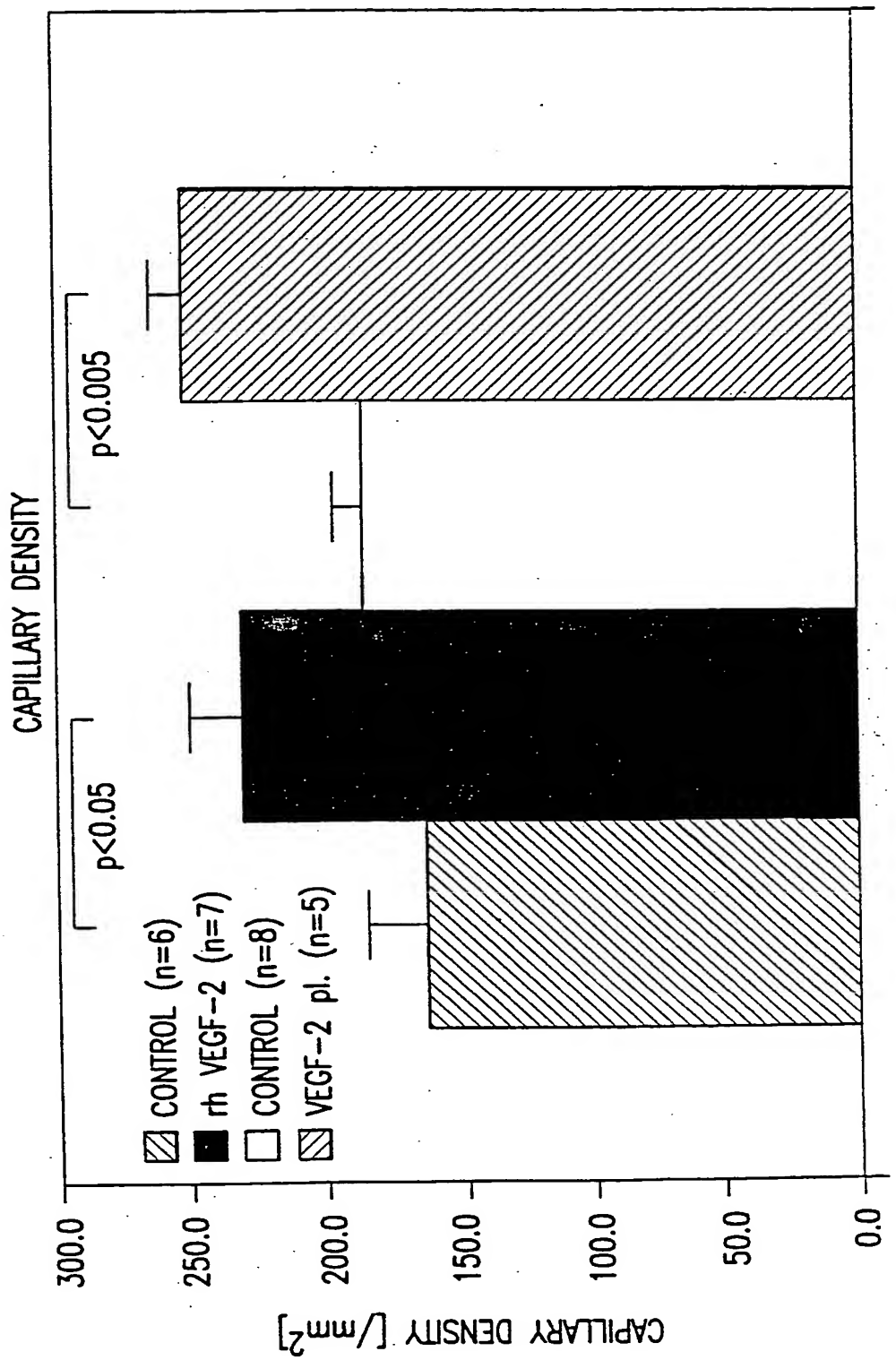

CAPILLARY DENSITY
p<0.005
p<0.05
CONTROL (n=6)
rh VEGF-2 (n=7)
CONTROL (n=8)
VEGF-2 pl. (n=5)
DAY 30
CAPILLARY DENSITY [/mm²]
300.0
250.0
200.0
150.0
100.0
50.0
0.0

FIG.25 O

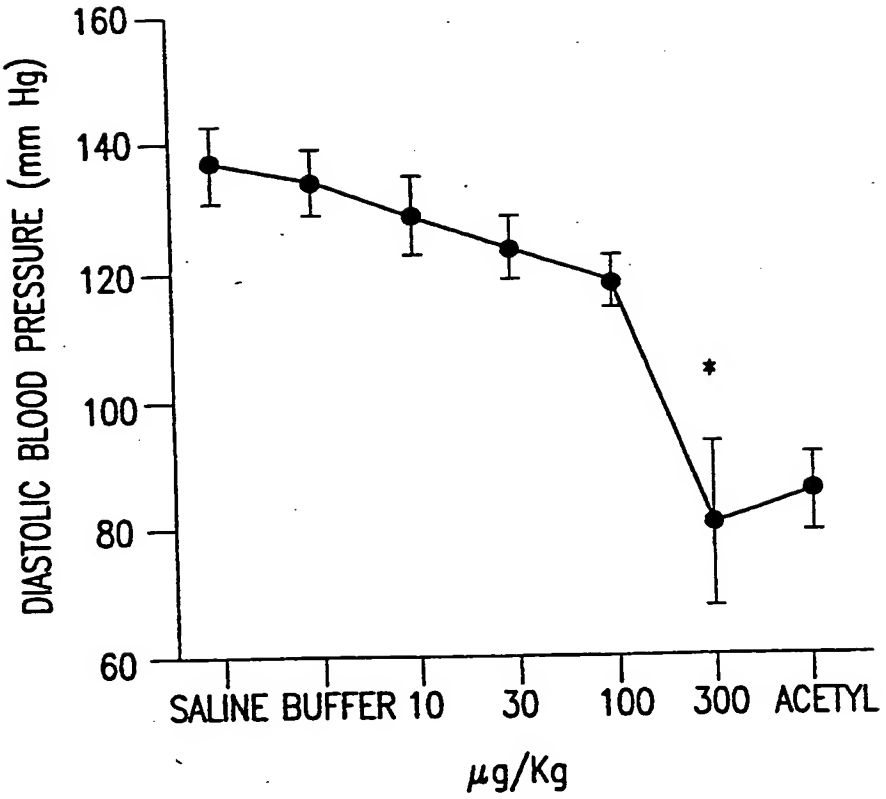


FIG.26A

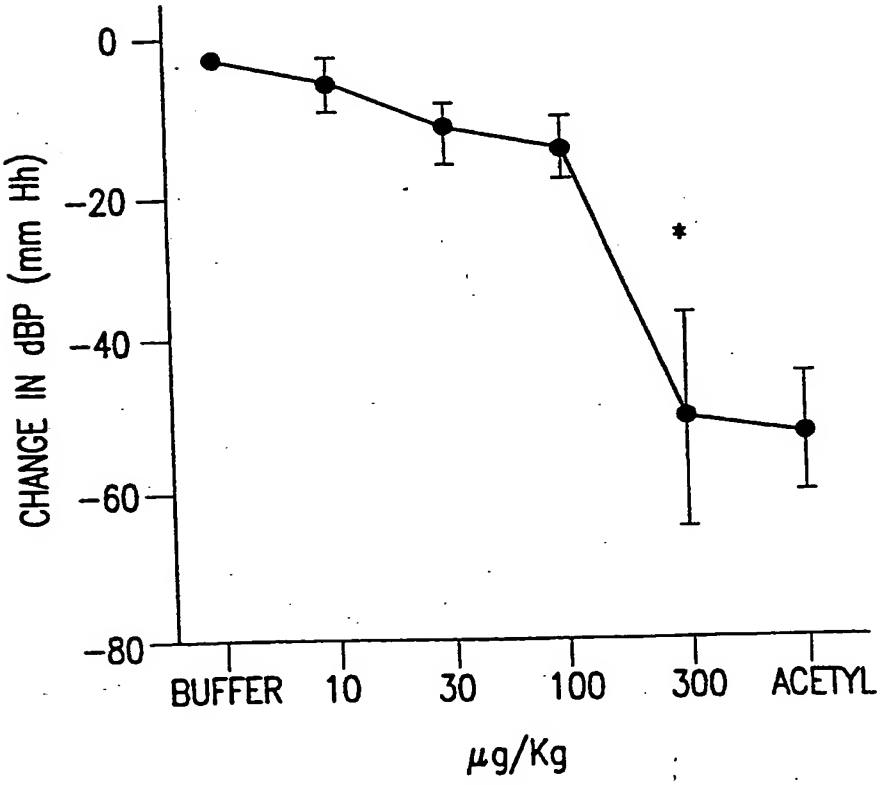


FIG.26B

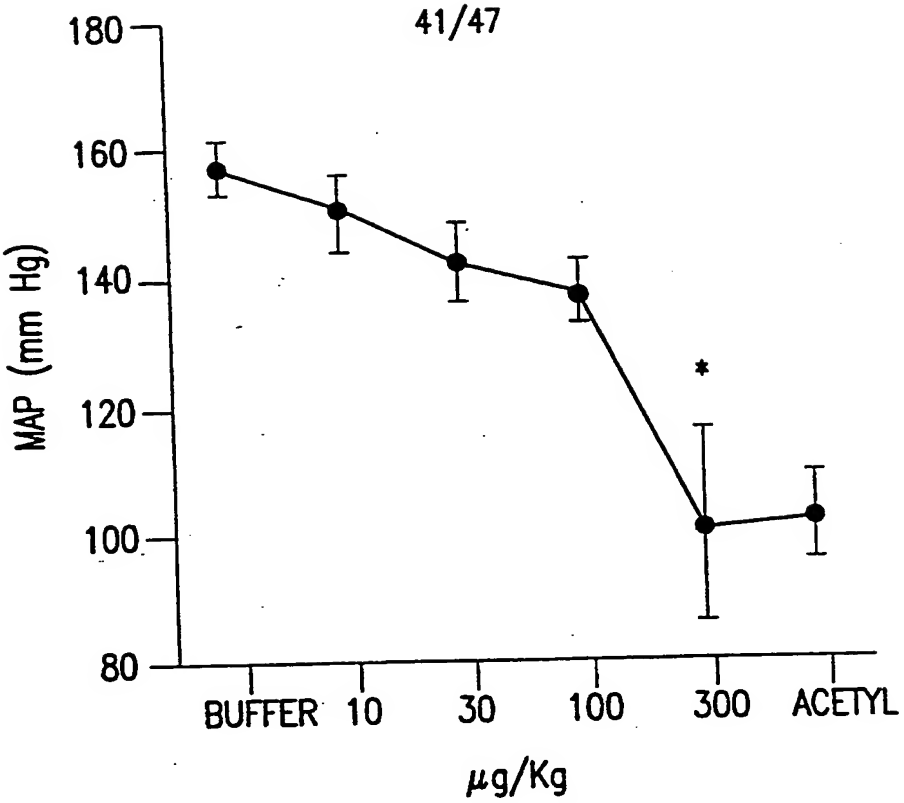


FIG.26C

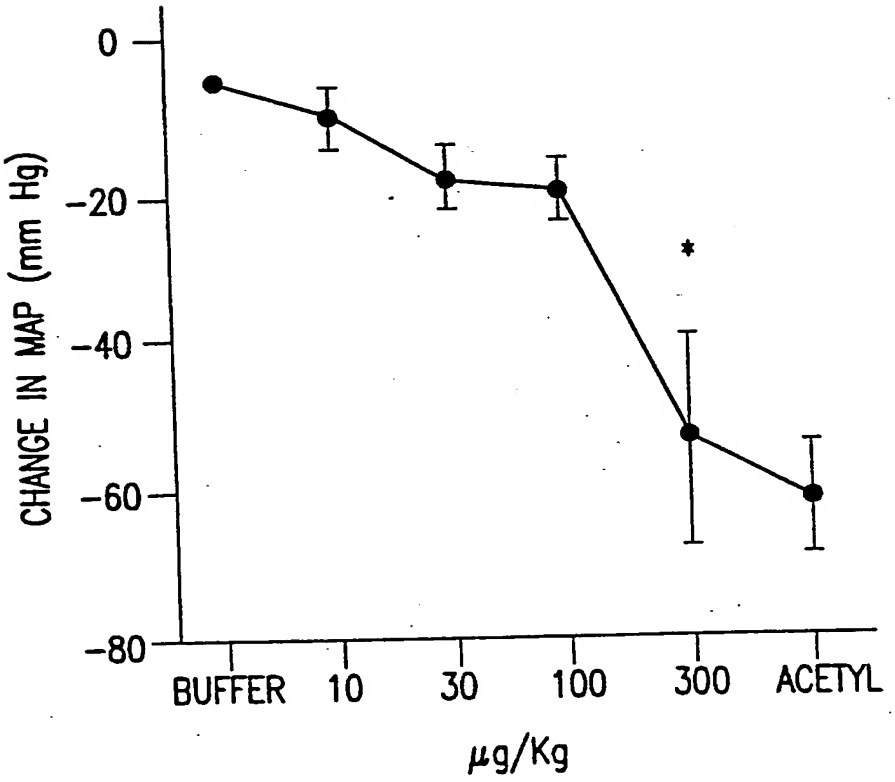


FIG.26D

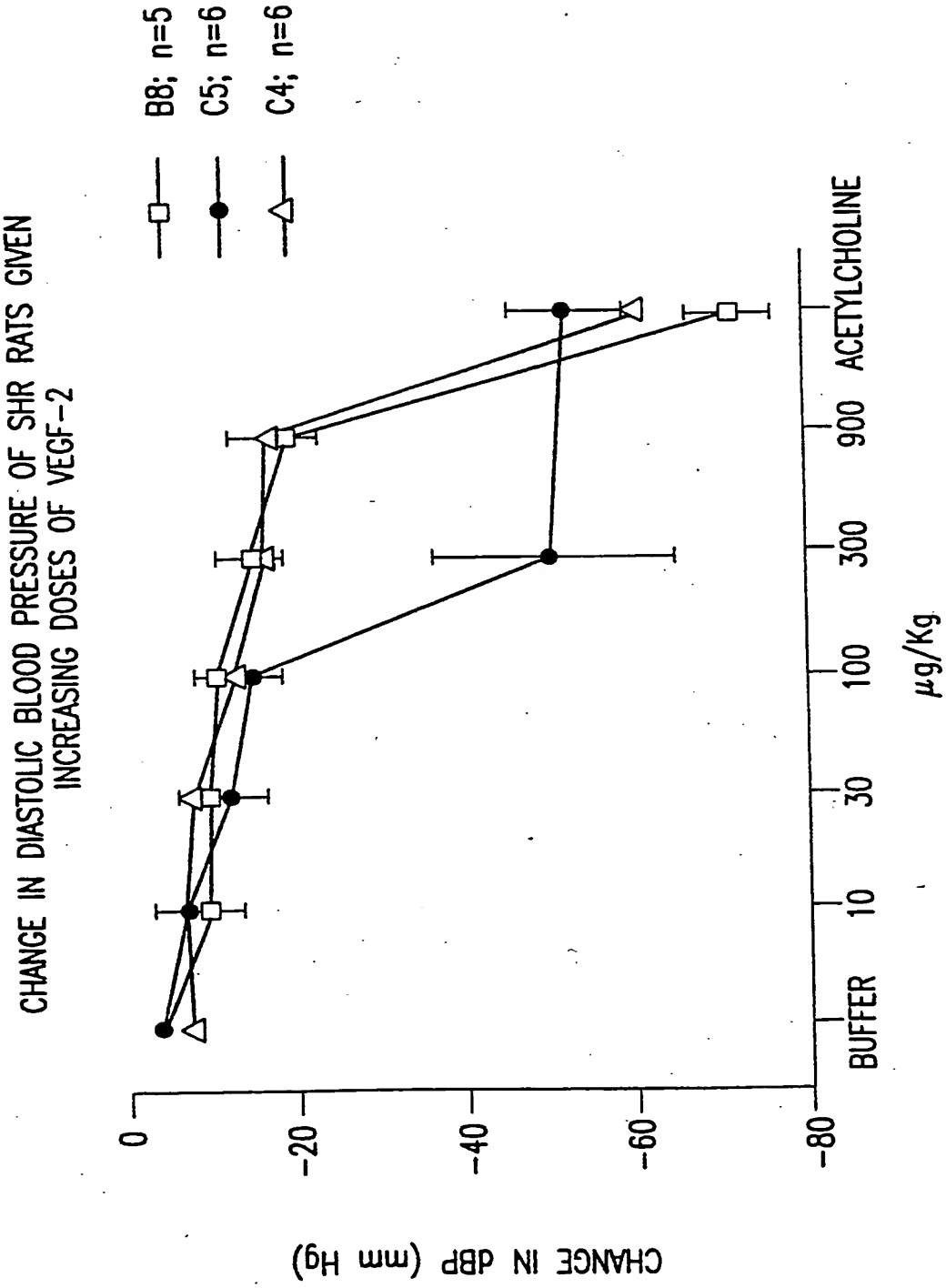

CHANGE IN DIASTOLIC BLOOD PRESSURE OF SHR RATS GIVEN INCREASING DOSES OF VEGF-2
B8; n=5
C5; n=6
C4; n=6
CHANGE IN dBP (mm Hg)
0
-20
-40
-60
-80
BUFFER
10
30
100
300
900
ACETYLCHOLINE
µg/Kg

FIG.26E

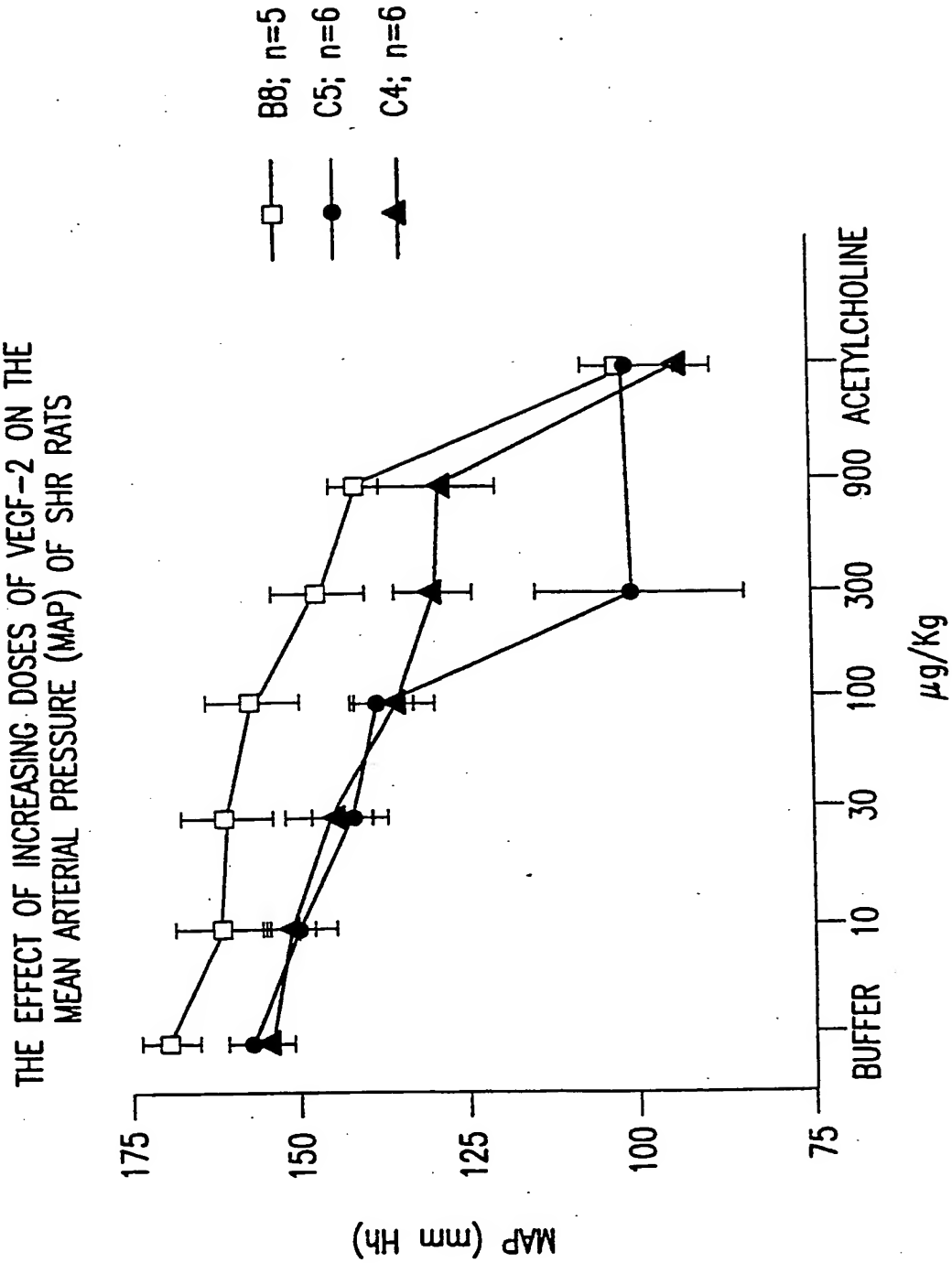

THE EFFECT OF INCREASING DOSES OF VEGF-2 ON THE MEAN ARTERIAL PRESSURE (MAP) OF SHR RATS
B8; n=5
C5; n=6
C4; n=6
MAP (mm Hg)
175
150
125
100
75
BUFFER
10
30
100
300
900
ACETYLCHOLINE
μg/Kg

FIG.26F

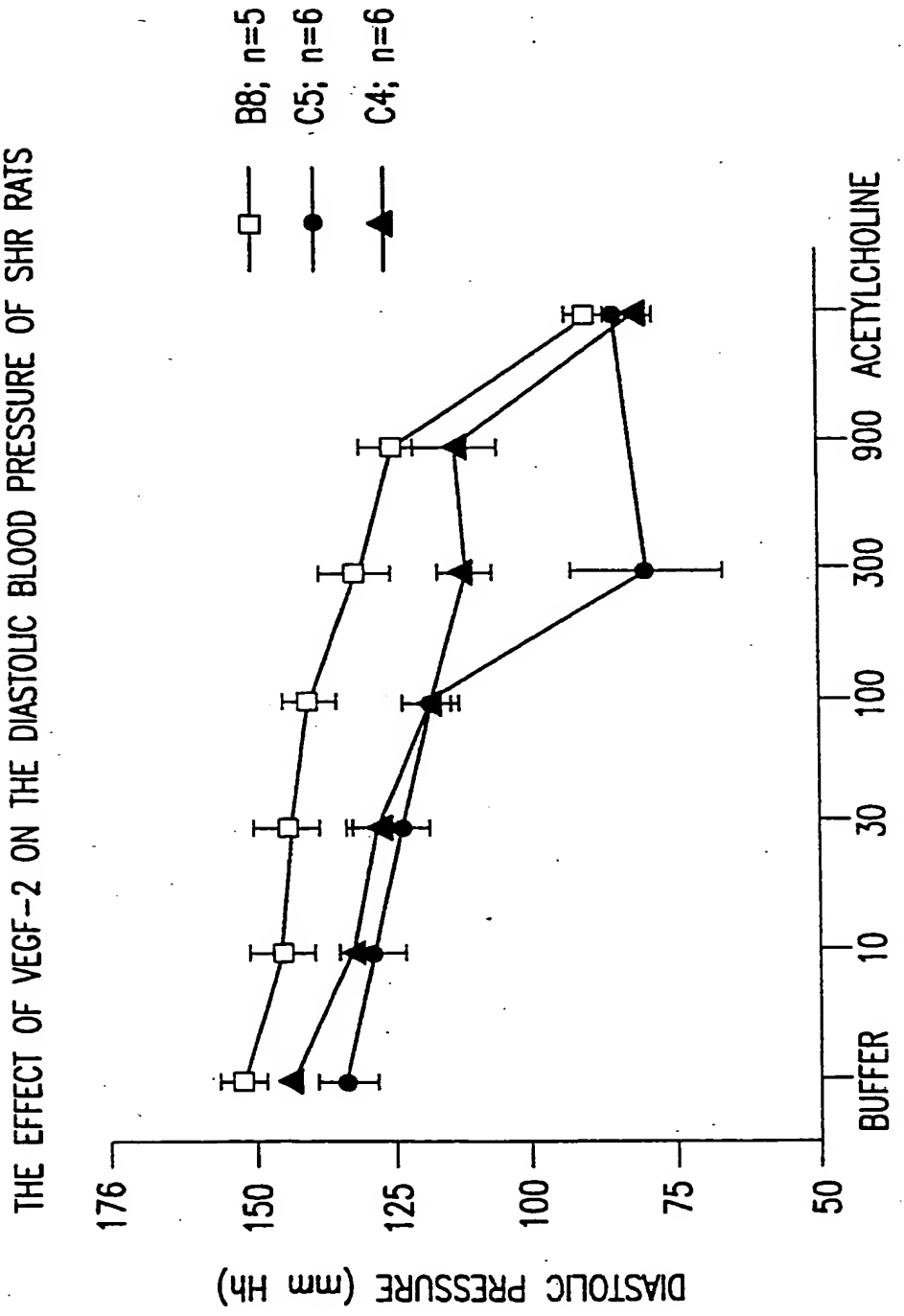

THE EFFECT OF VEGF-2 ON THE DIASTOLIC BLOOD PRESSURE OF SHR RATS
B8; n=5
C5; n=6
C4; n=6
DIASTOLIC PRESSURE (mm Hh)
176
150
125
100
75
50
BUFFER
10
30
100
300
900
ACETYLCHOLINE

FIG.26G

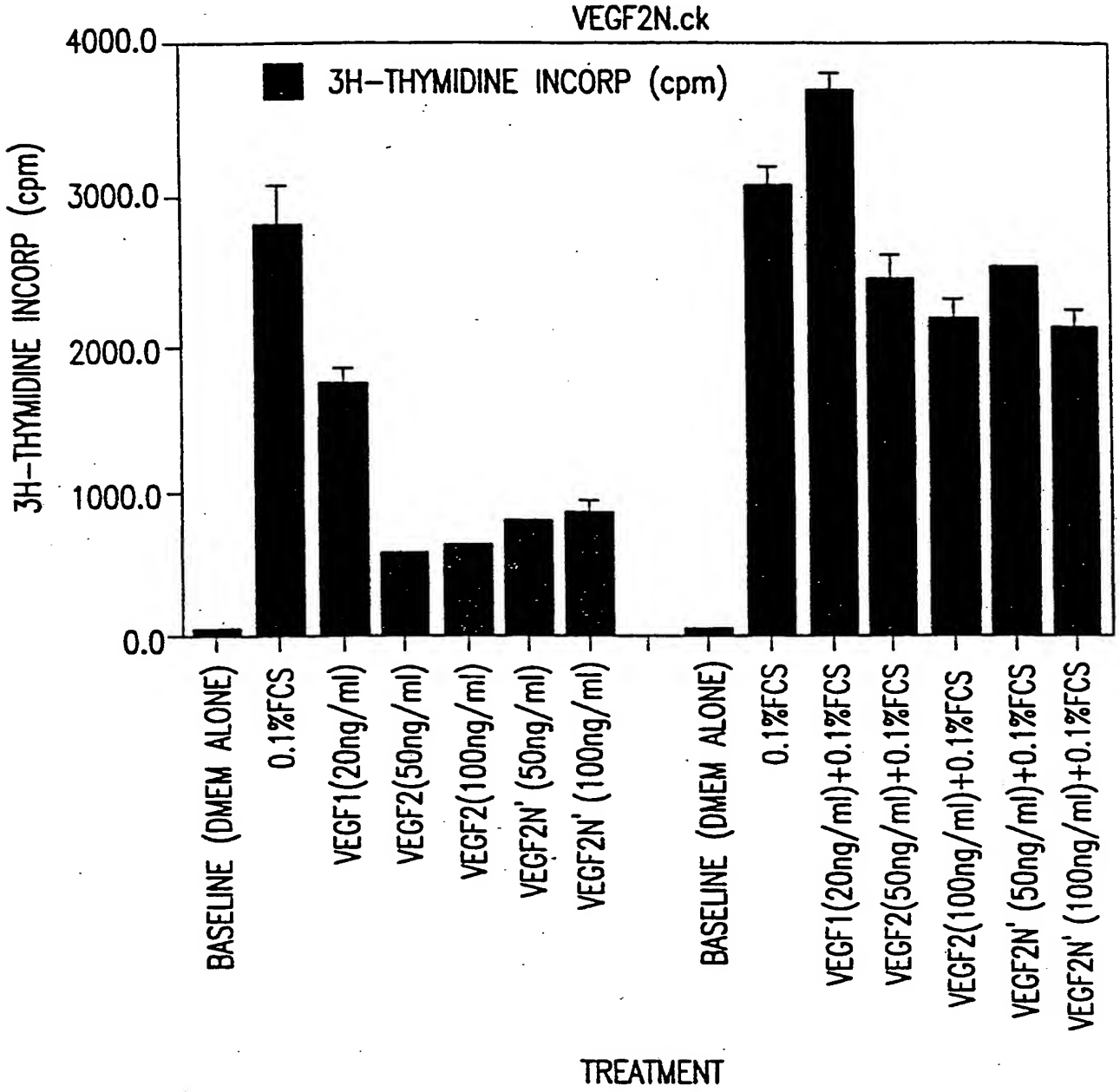

VEGF2N.ck
3H-THYMIDINE INCORP (cpm)
4000.0
3000.0
2000.0
1000.0
0.0
3H-THYMIDINE INCORP (cpm)
BASELINE (DMEM ALONE)
0.1%FCS
VEGF1(20ng/ml)
VEGF2(50ng/ml)
VEGF2(100ng/ml)
VEGF2N' (50ng/ml)
VEGF2N' (100ng/ml)
BASELINE (DMEM ALONE)
0.1%FCS
VEGF1(20ng/ml)+0.1%FCS
VEGF2(50ng/ml)+0.1%FCS
VEGF2(100ng/ml)+0.1%FCS
VEGF2N' (50ng/ml)+0.1%FCS
VEGF2N' (100ng/ml)+0.1%FCS
TREATMENT

FIG.27

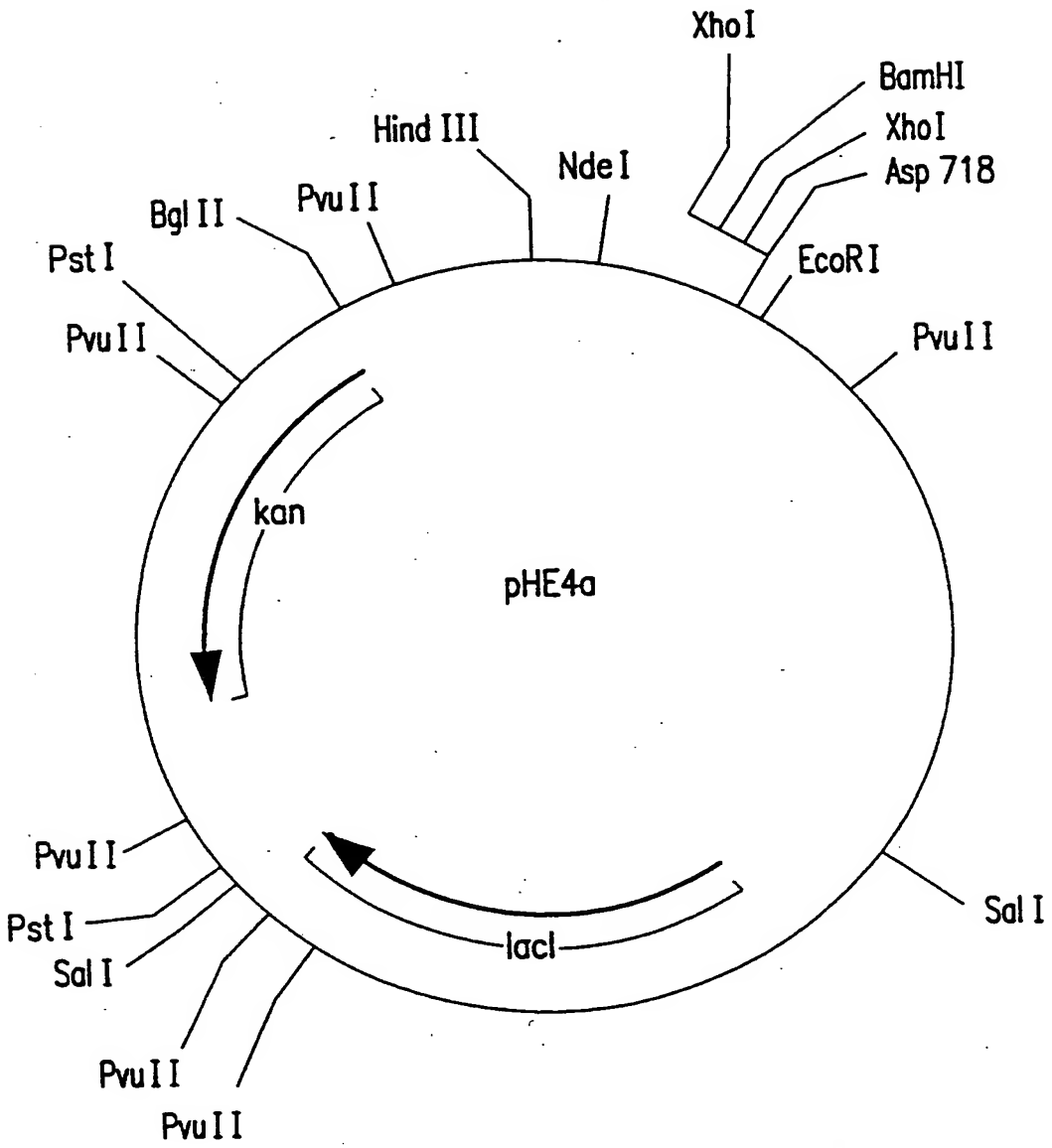

XhoI
BamHI
XhoI
Asp 718
EcoRI
PvuII
SalI
lacI
PvuII
PvuII
PvuII
SalI
PstI
PvuII
kan
pHE4a
PvuII
BglII
PstI
HindIII
NdeI

FIG.28

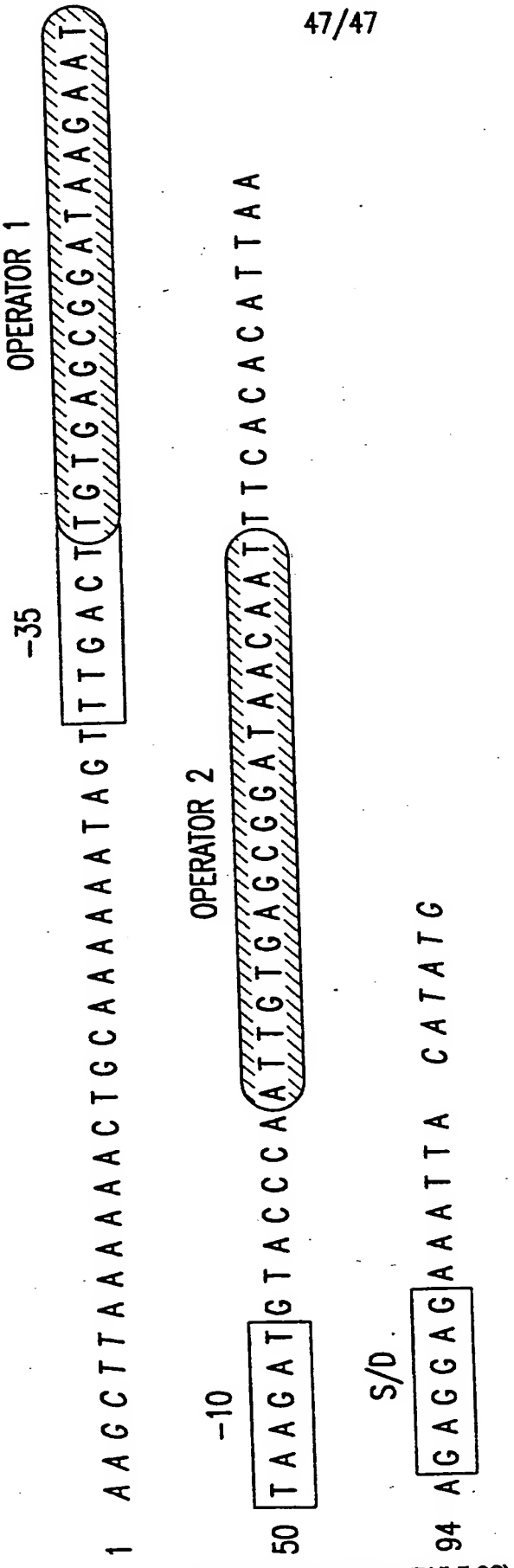

OPERATOR 1
-35
1 AAGCTTAAAAAACTGCAAAAATAGT TTGACT TGTGAGCGGATAACAAT
OPERATOR 2
-10
50 TAAGAT GTACCCA ATTGTGAGCGGATAACAAT TCACACATTAA
S/D
94 AGAGGAG AAATTA CATATG

FIG.29